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(54) Title: HUMAN AND MOUSE TARGETING PEPTIDES IDENTIFIED BY PHAGE DISPLAY

(57) Abstract: The present invention concerns methods and compositions for in vivo and in vitro targeting. A large number of targeting peptides directed towards human organs, tissues or cell types are disclosed. The peptides are of use for targeted delivery of therapeutic agents, including but not limited to gene therapy vectors. A novel class of gene therapy vectors is disclosed. Certain of the disclosed peptides have therapeutic use for inhibiting angiogenesis, inhibiting tumor growth, inducing apoptosis, inhibiting pregnancy or inducing weight loss. Methods of identifying novel targeting peptides in humans, as well as identifying endogenous receptor-ligand pairs are disclosed. Methods of identifying novel infectious agents that are causal for human disease states are also disclosed. A novel mechanism for inducing apoptosis is further disclosed.

HUMAN AND MOUSE TARGETING PEPTIDES IDENTIFIED BY PHAGE DISPLAY

BACKGROUND OF THE INVENTION

This application claims priority from U.S. Provisional Patent Application No. 60/231,266 filed September 8, 2000, and U.S. Patent Application No. 09/765,101, filed January 17, 2001. This invention was made with government support under grants DAMD 17-98-1-8041 and 17-98-1-8581 from the U.S. Army and grants 1R01CA78512-01A1, 1R1CA90810-01 and 1R01CA82976-01 from the National Institutes of Health. The government has certain rights in this invention.

1. Field of the Invention

The present invention concerns the fields of molecular medicine and targeted delivery of therapeutic agents. More specifically, the present invention relates to compositions and methods for identification and use of peptides that selectively target organs tissues or cell types *in vivo* or *in vitro*.

Description of Related Art

Therapeutic treatment of many disease states is limited by the systemic toxicity of the therapeutic agents used. Cancer therapeutic agents in particular exhibit a very low therapeutic index, with rapidly growing normal tissues such as skin and bone marrow affected at concentrations of agent that are not much higher than the concentrations used to kill tumor cells. Treatment of cancer and other organ, tissue or cell type confined disease states would be greatly facilitated by the development of compositions and methods for targeted delivery to a desired organ, tissue or cell type of a therapeutic agent.

Recently, an *in vivo* selection system was developed using phage display libraries to identify organ, tissue or cell type targeting peptides in a mouse model system. Phage display libraries expressing transgenic peptides on the surface of bacteriophage were initially developed to map epitope binding sites of

immunoglobulins (Smith and Scott, 1986, 1993). Such libraries can be generated by inserting random oligonucleotides into cDNAs encoding a phage surface protein, generating collections of phage particles displaying unique peptides in as many as 10^9 permutations. (Pasqualini and Ruoslahti, 1996, Arap et al, 1998a; Arap et al 1998b).

Intravenous administration of phage display libraries to mice was followed by the recovery of phage from individual organs (Pasqualini and Ruoslahti, 1996). Phage were recovered that were capable of selective homing to the vascular beds of different mouse organs, tissues or cell types, based on the specific targeting peptide sequences expressed on the outer surface of the phage (Pasqualini and Ruoslahti, 1996). A variety of organ and tumor-homing peptides have been identified by this method (Rajotte et al., 1998, 1999; Koivunen et al., 1999; Burg et al., 1999; Pasqualini, 1999). Each of those targeting peptides bound to different receptors that were selectively expressed on the vasculature of the mouse target tissue (Pasqualini, 1999; Pasqualini et al., 2000; Folkman, 1995; Folkman 1997). Tumor-homing peptides bound to receptors that were upregulated in the tumor angiogenic vasculature of mice (Brooks et al., 1994; Pasqualini et al., 2000). In addition to identifying individual targeting peptides selective for an organ, tissue or cell type (Pasqualini and Ruoslahti, 1996; Arap et al, 1998a; Koivunen et al., 1999), this system has been used to identify endothelial cell surface markers that are expressed in mice *in vivo* (Rajotte and Ruoslahti, 1999).

Attachment of therapeutic agents to targeting peptides resulted in the selective delivery of the agent to a desired organ, tissue or cell type in the mouse model system. Targeted delivery of chemotherapeutic agents and proapoptotic peptides to receptors located in tumor angiogenic vasculature resulted in a marked increase in therapeutic efficacy and a decrease in systemic toxicity in tumor-bearing mouse models (Arap et al., 1998a, 1998b; Ellerby et al., 1999).

In some cases, previous *in vivo* methods for phage display screening resulted in relatively high backgrounds of non-specific phage binding. This was particularly true for tissues belonging to the reticuloendothelial system. A need exists for improved

methods of phage display that decrease non-specific phage binding, while retaining specific interactions between targeting peptides and cell receptors. A need also exists to target receptors for specific cell populations within an organ, tissue or cell type. In many cases, tissues or organs may contain highly heterologous populations of different cell types. A need exists to be able to target phage display screening to specific cell populations.

A need also exists to identify receptor-ligand pairs in organs and tissues. Previous attempts to identify targeted receptors and ligands binding to receptors have largely targeted a single ligand at a time for investigation. Identification of previously unknown receptors and previously uncharacterized ligands has been a very slow and laborious process. Such novel receptors and ligands may provide the basis for new therapies for a variety of disease states, such as is diabetes mellitus, inflammatory disease, arthritis, atherosclerosis, cancer, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease.

SUMMARY OF THE INVENTION

The present invention solves a long-standing need in the art by providing compositions and methods for the identifying and using targeting peptides that are selective for organs, tissues or specific cell types. In certain embodiments, the methods concern Biopanning and Rapid Analysis of Selective Interactive Ligands (BRASIL), a novel method for phage display that results in decreased background of non-specific phage binding, while retaining selective binding of phage to cell receptors. In preferred embodiments, targeting peptides are identified by exposing a subject to a phage display library, collecting samples of one or more organs, tissues or cell types, separating the samples into isolated cells or small clumps of cells suspended in an aqueous phase, layering the aqueous phase over an organic phase, centrifuging the two phases so that the cells are pelleted at the bottom of a centrifuge tube and collecting phage from the pellet. In an even more preferred embodiment, the organic phase is dibutylphtalate.

In other embodiments, phage that bind to a target organ, tissue or cell type, for example to placenta, may be pre-screened or post-screened against a subject lacking that organ, tissue or cell type. Phage that bind to the subject lacking the target organ, tissue or cell type are removed from the library prior to screening in subjects possessing the organ, tissue or cell type. In preferred embodiments, the organ, tissue or cell type is placenta or adipose tissue.

In preferred embodiments, targeting phage may be recovered from specific cell types or sub-types present in an organ or tissue after selection of the cell type by PALM (Positioning and Ablation with Laser Microbeams). PALM allows specific cell types to be selected from, for example, a thin section of an organ or tissue. Phage may be recovered from the selected sample.

In another embodiment, a phage display library displaying the antigen binding portions of antibodies from a subject is prepared, the library is screened against one or more antigens and phage that bind to the antigens are collected. In more preferred embodiments, the antigen is a targeting peptide.

In certain embodiments, the methods and compositions may be used to identify one or more receptors for a targeting peptide. In alternative embodiments, the compositions and methods may be used to identify naturally occurring ligands for known or newly identified receptors.

In some embodiments, the methods may comprise contacting a targeting peptide to an organ, tissue or cell containing a receptor of interest, allowing the peptide to bind to the receptor, and identifying the receptor by its binding to the peptide. In preferred embodiments, the targeting peptide contains at least three contiguous amino acids selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:251. In other preferred embodiments, the targeting peptide comprises a portion of an antibody against the receptor. In alternative embodiments, the targeting peptide may contain a random amino acid sequence. The skilled artisan will realize that the contacting step

can utilize intact organs, tissues or cells, or may alternatively utilize homogenates or detergent extracts of the organs, tissues or cells. In certain embodiments, the cells to be contacted may be genetically engineered to express a suspected receptor for the targeting peptide. In a preferred embodiment, the targeting peptide is modified with a reactive moiety that allows its covalent attachment to the receptor. In a more preferred embodiment, the reactive moiety is a photoreactive group that becomes covalently attached to the receptor when activated by light. In another preferred embodiment, the peptide is attached to a solid support and the receptor is purified by affinity chromatography. In other preferred embodiments, the solid support comprises magnetic beads, Sepharose beads, agarose beads, a nitrocellulose membrane, a nylon membrane, a column chromatography matrix, a high performance liquid chromatography (HPLC) matrix or a fast performance liquid chromatography (FPLC) matrix. In certain embodiments, the targeting peptide inhibits the activity of the receptor upon binding to the receptor. The skilled artisan will realize that receptor activity can be assayed by a variety of methods known in the art, including but not limited to catalytic activity and binding activity. In another preferred embodiment, the receptor is an endostatin receptor, a metalloprotease or an aminopeptidase.

In alternative embodiments, one or more ligands for a receptor of interest may be identified by the disclosed methods and compositions. One or more targeting peptides that mimic part or all of a naturally occurring ligand may be identified by phage display and biopanning *in vivo* or *in vitro*. A naturally occurring ligand may be identified by homology with a single targeting peptide that binds to the receptor, or a consensus motif of sequences that bind to the receptor. In other alternative embodiments, an antibody may be prepared against one or more targeting peptides that bind to a receptor of interest. Such antibodies may be used for identification or immunoaffinity purification of the native ligand.

In certain embodiments, the targeting peptides of the present invention are of use for the selective delivery of therapeutic agents, including but not limited to gene therapy vectors and fusion proteins, to specific organs, tissues or cell types. The skilled

artisan will realize that the scope of the claimed methods of use include any disease state that can be treated by targeted delivery of a therapeutic agent to a desired organ, tissue or cell type. Although such disease states include those where the diseased cells are confined to a specific organ, tissue or cell type, such as non-metastatic cancer, other disease states may be treated by an organ, tissue or cell type-targeting approach.

One embodiment of the present invention concerns isolated peptides of 100 amino acids or less in size, comprising at least 3 contiguous amino acids of a targeting peptide sequence, selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:251.

In a preferred embodiment, the isolated peptide is 50 amino acids or less, more preferably 30 amino acids or less, more preferably 20 amino acids or less, more preferably 10 amino acids or less, or even more preferably 5 amino acids or less in size. In other preferred embodiments, the isolated peptide of claim 1 comprises at least 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14,15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or 25 contiguous amino acids of a targeting peptide sequence, selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:251.

In certain embodiments, the isolated peptide is attached to a molecule. In preferred embodiments, the attachment is a covalent attachment. In additional embodiments, the molecule is a drug, a chemotherapeutic agent, a radioisotope, a pro-apoptosis agent, an anti-angiogenic agent, a hormone, a cytokine, a growth factor, a cytotoxic agent, a peptide, a protein, an antibiotic, an antibody, a Fab fragment of an antibody, a survival factor, an anti-apoptotic factor, a hormone antagonist, an imaging agent, a nucleic acid or an antigen. Those molecules are representative only. Molecules within the scope of the present invention include virtually any molecule that may be attached to a targeting peptide and administered to a subject. In preferred embodiments, the pro-aptoptosis agent is gramicidin, magainin, mellitin, defensin,

cecropin, $(KLAKLAK)_2$ (SEQ ID NO:1), $(KLAKKLA)_2$ (SEQ ID NO:2), $(KAAKKAA)_2$ (SEQ ID NO:3) or $(KLGKKLG)_3$ (SEQ ID NO:4). In other preferred embodiments, the anti-angiogenic agent is angiostatin5, pigment epithelium-drived factor, angiotensin, laminin peptides, fibronectin peptides, plasminogen activator inhibitors, tissue metalloproteinase inhibitors, interferons, interleukin 12, platelet factor 4, IP-10, Gro-ß, thrombospondin, 2-methoxyoestradiol, proliferin-related protein, carboxiamidotriazole, CM101, Marimastat, pentosan polysulphate, angiopoietin 2 (Regeneron), interferon-alpha, herbimycin A, PNU145156E, 16K prolactin fragment, Linomide, thalidomide, pentoxifylline, genistein, TNP-470, endostatin, paclitaxel, docetaxel, polyamines, a proteasome inhibitor, a kinase inhibitor, a signaling inhibitor (SU5416, SU6668, Sugen, South San Francisco, CA), accutin, cidofovir, vincristine, bleomycin, AGM-1470, platelet factor 4 or minocycline. In further preferred embodiments, the cytokine is interleukin 1 (IL-1), IL-2, IL-5, IL-10, IL-11, IL-12, IL-18, interferon-γ (IF-γ), IF-α, IF-ß, tumor necrosis factor-α (TNF-α), or GM-CSF (granulocyte macrophage colony stimulating factor). Such examples are representative only and are not intended to exclude other pro-apoptosis agents, anti-angiogenic agents or cytokines known in the art.

In other embodiments, the isolated peptide is attached to a macromolecular complex. In preferred embodiments, the attachment is a covalent attachment. In other preferred embodiments, the macromolecular complex is a virus, a bacteriophage, a bacterium, a liposome, a microparticle, a magnetic bead, a yeast cell, a mammalian cell, a cell or a microdevice. These are representative examples only. Macromolecular complexes within the scope of the present invention include virtually any macromolecular complex that may be attached to a targeting peptide and administered to a subject. In other preferred embodiments, the isolated peptide is attached to a eukaryotic expression vector, more preferably a gene therapy vector.

In another embodiment, the isolated peptide is attached to a solid support, preferably magnetic beads, Sepharose beads, agarose beads, a nitrocellulose membrane, a nylon membrane, a column chromatography matrix, a high performance liquid

chromatography (HPLC) matrix or a fast performance liquid chromatography (FPLC) matrix.

Additional embodiments of the present invention concern fusion proteins comprising at least 3 contiguous amino acids of a sequence selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:251.

Certain other embodiments concern compositions comprising the claimed isolated peptides or fusion proteins in a pharmaceutically acceptable carrier. Further embodiments concern kits comprising the claimed isolated peptides or fusion proteins in one or more containers.

Other embodiments concern methods of targeted delivery comprising selecting a targeting peptide for a desired organ, tissue or cell type, attaching said targeting peptide to a molecule, macromolecular complex or gene therapy vector, and providing said peptide attached to said molecule, complex or vector to a subject. Preferably, the targeting peptide is selected to include at least 3 contiguous amino acids from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:251. In certain preferred embodiments, the organ, tissue or cell type is bone marrow, lymph node, prostate cancer or prostate cancer that has metastasized to bone marrow. In other preferred embodiments, the molecule attached to the targeting peptide is a chemotherapeutic agent, an antigen or an imaging agent. The skilled artisan will realize that within the scope of the present invention any organ, tissue or cell type can be targeted for delivery, using targeting peptides attached to any molecule, macromolecular complex or gene therapy vector.

Other embodiments of the present invention concern isolated nucleic acids of 300 nucleotides or less in size, encoding a targeting peptide. In preferred embodiments, the isolated nucleic acid is 250, 225, 200, 175, 150, 125, 100, 75, 50, 40, 30, 20 or even 10 nucleotides or less in size. In other preferred embodiments, the isolated nucleic acid

is incorporated into a eukaryotic or a prokaryotic expression vector. In even more preferred embodiments, the vector is a plasmid, a cosmid, a yeast artificial chromosome (YAC), a bacterial artificial chromosome (BAC), a virus or a bacteriophage. In other preferred embodiments, the isolated nucleic acid is operatively linked to a leader sequence that localizes the expressed peptide to the extracellular surface of a host cell.

Additional embodiments of the present invention concern methods of treating a disease state comprising selecting a targeting peptide that targets cells associated with the disease state, attaching one or more molecules effective to treat the disease state to the peptide, and administering the peptide to a subject with the disease state. Preferably, the targeting peptide includes at least three contiguous amino acids selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:251. In preferred embodiments the disease state is diabetes mellitus, inflammatory disease, arthritis, atherosclerosis, cancer, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease.

Another embodiment of the present invention concerns compositions and methods of use of tumor targeting peptides against cancers. Tumor targeting peptides identified by the methods disclosed in the instant application may be attached to therapeutic agents, including but not limited to molecules or macromolecular assemblages and administered to a subject with cancer, providing for increased efficacy and decreased systemic toxicity of the therapeutic agent. Therapeutic agents within the scope of the present invention include but are not limited to chemotherapeutic agents, radioisotopes, pro-apoptosis agents, cytotoxic agents, cytostatic agents and gene therapy vectors. Targeted delivery of such therapeutic agents to tumors provides a significant improvement over the prior art for increasing the delivery of the agent to the tumor, while decreasing the inadvertent delivery of the agent to normal organs and tissues of the subject. In a preferred embodiment, the tumor targeting peptide is incorporated into the capsule of a phage gene therapy vector to target delivery of the phage to angiogenic endothelial cells in tumor blood vessels.

Certain embodiments concern methods of obtaining antibodies against an antigen. In preferred embodiments, the antigen comprises one or more targeting peptides. The targeting peptides are prepared and immobilized on a solid support, serum containing antibodies is added and antibodies that bind to the targeting peptides are collected.

BRIEF DESCRIPTION OF THE DRAWINGS

The following drawings form part of the present specification and are included to further demonstrate certain aspects of the present invention. The invention may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

FIG. 1. Validation of placenta homing phage. Phage bearing targeting peptides identified in Example 3 were injected into pregnant mice and their recovery from placenta was compared to control fd-tet phage without targeting sequences. The placenta homing phage clones were: PA - TPKTSVT (SEQ ID NO:39), PC - RAPGGVR (SEQ ID NO:41), PE - LGLRSVG (SEQ ID NO:44), PF - YIRPFTL (SEQ ID NO:43).

FIG. 2. Validation of adipose homing peptides. Phage bearing targeting peptides identified in Example 4 were injected into pregnant mice and their recovery from adipose tissue was compared to control fd-tet phage without targeting sequences.

FIG. 3. Spleen targeting *in vitro* using BRASIL. Binding of Fab clones #2, #6, #10, #12 and control Fab clone NPC-3TT was compared to binding of control Fd-tet phage.

FIG. 4. Spleen targeting *in vitro* using BRASIL. Binding of Fab clones #2, #6, #10, #12 and control Fab clone NPC-3TT were directly compared to each other.

FIG. 5. Spleen targeting *in vivo* using BRASIL. Binding of Fab clones #2, #6, #10, #12 was compared to binding of Fd-tet phage.

FIG. 6. Spleen targeting *in vivo* using BRASIL. Binding of Fab clone #10 to spleen tissue was compared to binding of Fab control clone NPC-3TT and Fd-tet phage.

FIG. 7. Binding of Fab clone #10 to spleen *versus* bone marrow in comparison to Fd-tet phage.

FIG. 8. Binding of Fab clones from an anti-Karposi's sarcoma library to angiogenic retina.

FIG. 9. Binding of ß3 cytoplasmic domain-selected phage to immobilized proteins. GST fusion proteins or GST alone were coated on microtiter wells at 10 μg/ml and used to bind phage expressing endostatin targeting peptides. Each phage is identified by the peptide sequence it displayed: GLDTYRGSP (SEQ ID NO:96); YDWWYPWSW (SEQ ID NO:95); CLRQSYSYNC (SEQ ID NO:104); SDNRYIGSW (SEQ ID NO:97); CEQRQTQEGC (SEQ ID NO:93); CFQNRC (SEQ ID NO:102). The data represent the mean colony counts from triplicate wells, with standard error of less than 10% of the mean.

FIG. 10. Binding of ß5 cytoplasmic domain-selected phage to immobilized proteins. GST fusion proteins or GST alone were coated on microtiter wells at 10 μg/ml and used to bind phage expressing endostatin binding peptides. Each phage is identified by the peptide sequence it displayed: (A) DEEGYYMMR (SEQ ID NO:110); (B) KQFSYRYLL (SEQ ID NO:111); (C) CEPYWDGWFC (SEQ ID NO:106); (D) VVISYSMPD (SEQ ID NO:112); and (E) CYIWPDSGLC (SEQ ID NO:105). The data represent the mean colony counts from triplicate wells, with standard error less than 10% of the mean.

FIG. 11. Binding of the cytoplasmic-domain binding phage to ß3 immobilized protein and inhibition with the synthetic peptide. Phage were incubated on wells coated with GST-ß3cyto in the presence of increasing concentrations of the corresponding synthetic peptide or a control peptide. The data represent the mean colony counts from triplicate wells, with standard error less than 10% of the mean.

FIG. 12. Binding of the cytoplasmic-domain binding phage to ß5 immobilized protein and inhibition with the synthetic peptide. Phage were incubated on wells coated with GST-ß5cyto in the presence of increasing concentrations of the corresponding synthetic peptide or a control peptide. The data represent the mean colony counts from triplicate wells, with standard error less than 10% of the mean.

FIG. 13. Binding of phage to immobilized ß3-GST and β5-GST after phosphorylation. Phage were phosphorylated with Fyn kinase. Insertless phage were used as a control. Phage were incubated on wells coated with GST-ß3cyto or GST-ß3cyto. The data represent the mean colony counts from triplicate wells, with standard error less than 10% of the mean.

FIG. 14. Binding of phage to immobilized GST fusion proteins after phosphorylation. Phages were phosphorylated with Fyn kinase. Insertless phage was used as a control. Phage were incubated on wells coated with GST-cytoplasmic domains. The data represent the mean of colony counts from triplicate wells, with standard error less than 10% of the mean.

FIG. 15. Effect of integrin cytoplasmic domain binding peptides on cell proliferation. Serum-deprived cells were cultured for 24 h.and the proliferation was determined by [^{3}H] thymidine (1μCi/ml) uptake measurements. In a positive control, VEGF was added back to serum-starved cells. Each experiment was performed three times with triplicates, and the results were expressed as the mean +/- SD.

FIG. 16. Effect of penetratin peptide chimeras on endothelial cell migration. Cell migration assay were performed in a 48-well microchemotaxis chamber. Five random high-power fields (magnitude 40×) were counted in each well. The results show that both β3-integrin cytoplasmic domain binding peptides (Y-18 and TYR-11) increase cell migration while penetratin does not affect the cells.

FIG. 17. Penetratin peptide chimera binding to the ß5 cytoplasmic domain induces programmed cell death. 10^6 HUVEC cells were harvested in complete media

and 15 μM penetratin peptide chimeras were added to the cells. After four, eight and twelve hours the cells were stained with Propidium Iodide (PI) and induction of apoptosis was analyzed by cytometric analysis. a) Profile obtained with starved cells after 24 h. b) Confluent cells in complete media. c) 15 μM of penetratin after four hours. d) 15μM of VISY-penetratin chimera after four hours. Cells analyzed after eight and twelve hours showed similar profiles for the percentage of G_0/G_1.

FIG. 18. Specificity of the antibodies raised against ß3- or ß5-selected phage (ELISA). Increasing dilutions of sera obtained after three immunizations with GLDTYRGSP (SEQ ID NO:96) or SDNRYIGSW (SEQ ID NO:97) conjugated to KLH were incubated on microtiterwells coated with 10 μg of SDNRYIGSW (SEQ ID NO:97, Y-18), GLDTYRGSP (SEQ ID NO:96, TYR-11) or control peptides. Preimmunesera were used as controls. After incubation with HRPgoat anti-rabbit, OD was measured at 405 nm. The data represent the means from triplicate wells, with standard error less than 10%.

FIG. 19. Specificity of the antibodies raised against ß3- or ß5-selected phage (ELISA). Sera obtained after three immunizations with SDNRYIGSW (SEQ ID NO:97, Y-18) or GLDTYRGSP (SEQ ID NO:96, TYR-11) conjugated to KLH were incubated in microtiter wells coated with 10 μg of TYR-11 or Y-18. GLDTYRGSP (SEQ ID NO:96) or SDNRYIGSW (SEQ ID NO:97) and control peptides were added in solution. After incubation with HRP goat anti-rabbit, OD was measured at 405 nm. The data represent the means from triplicate wells, with standard error less than 10%. Peptides added in solution specifically block the reactivity with the immobilized peptides.

FIG. 20A. Competitive binding of Annexin V to β5 integrin with VISY peptide. Binding assays were performed by ELISA.

FIG. 20B. Relative levels of binding of anti-Annexin V antibody to purified Annexin V protein and VISY peptide.

FIG. 21. Chimeric peptide containing VISY peptide linked to penetratin (antennapedia) induces apoptosis. VISY induced apoptosis was inhibited by addition of a caspase inhibitor (zVAD).

FIG. 22. APA-binding phage specifically bind tumors. Equal amounts of phage were injected into the tail veins of mice bearing MDA-MB-435-derived tumors and phage were recovered after perfusion. Mean values for phage recovered from the tumor or control tissue (brain) and the standard error from triplicate platings are shown.

FIG. 23. CPRECESIC (SEQ ID NO:123) is a specific inhibitor of APA activity. APA enzyme activity was assayed in the presence of increasing concentrations of either GACVRLSACGA (SEQ ID NO:124) (control) or CPRECESIC (SEQ ID NO:123) peptide. The IC_{50} for APA inhibition by CPRECESIC (SEQ ID NO:123) was estimated at 800 μM. Error bars are the standard error of the means of triplicate wells. The experiment was repeated three times with similar results.

FIG. 24. CPRECESIC (SEQ ID NO:123) inhibits HUVEC migration. HUVECs were stimulated with VEGF-A (10 ng/ml). The assay was performed in a Boyden microchemotaxis chamber, and cells were allowed to migrate through an 8-μm pore filter for 5 h at 37°C. GACVRLSACGA (SEQ ID NO:124) (control) and CPRECESIC (SEQ ID NO:123) peptides were tested at 1 mM concentration. Migrated cells were stained and five high-power fields (magnitude 100×) for each microwell were counted. Error bars are the standard error of the means of triplicate microwells.

FIG. 25. CPRECESIC (SEQ ID NO:123) inhibits HUVEC proliferation. Cells were stimulated with VEGF-A (10 ng/ml), and growth was evaluated at the indicated times by a colorimetric assay based on crystal violet staining. Error bars are the standard error of the means of triplicate wells. Each experiment was repeated at least twice with similar results.

FIG. 26. Protocol for *in vivo* biopanning for phage targeted in mouse pancreas, kidneys, liver, lungs and adrenal gland.

FIG. 27. Protocol for recovery of phage by infection of *E. coli* or recovery of phage DNA by amplification and subcloning.

FIG. 28. Pancreatic islet targeting peptides and homologous proteins. Candidate endogenous proteins mimicked by the pancreatic islet targeting peptides CVSNPRWKC (SEQ ID NO:197), CVPRRWDVC (SEQ ID NO:194), CQHTSGRGC (SEQ ID NO:195) and CRARGWLLC (SEQ ID NO:196), identified by standard homology searches.

FIG. 29. Pancreatic islet targeting peptides and homologous proteins. Candidate endogenous proteins mimicked by the pancreatic islet targeting peptides CGGVHALRC (SEQ ID NO:175), CFNRTWIGC (SEQ ID NO:198) and CWSRQGGC (SEQ ID NO:200, identified by standard homology searches.

FIG. 30. Pancreatic islet targeting peptides and homologous proteins. Candidate endogenous proteins mimicked by the pancreatic islet targeting peptides CLASGMDAC (SEQ ID NO:204), CHDERTGRC (SEQ ID NO:205), CAHHALMEC (SEQ ID NO:206) and CMQGARTSC (SEQ ID NO:208), identified by standard homology searches.

FIG. 31. Pancreatic islet targeting peptides and homologous proteins. Candidate endogenous proteins mimicked by the pancreatic islet targeting peptides CHVLWSTRC (SEQ ID NO:201), CMSSPGVAC (SEQ ID NO:203) and CLGLLMAGC (SEQ ID NO:202), identified by standard homology searches.

DESCRIPTION OF ILLUSTRATIVE EMBODIMENTS

As used herein in the specification, "a" or "an" may mean one or more. As used herein in the claim(s), in conjunction with the word "comprising," the words "a" or "an" may mean one or more than one. As used herein "another" may mean at least a second or more of an item.

A "targeting peptide" is a peptide comprising a contiguous sequence of amino acids, that is characterized by selective localization to an organ, tissue or cell type.

Selective localization may be determined, for example, by methods disclosed below, wherein the putative targeting peptide sequence is incorporated into a protein that is displayed on the outer surface of a phage. Administration to a subject of a library of such phage that have been genetically engineered to express a multitude of such targeting peptides of different amino acid sequence is followed collection of one or more organs, tissues or cell types from the subject and identification of phage found in that organ, tissue or cell type. A phage expressing a targeting peptide sequence is considered to be selectively locallized to a tissue or organ if it exhibits greater binding in that tissue or organ compared to a control tissue or organ. Preferably, selective localization of a targeting peptide should result in a two-fold or higher enrichment of the phage in the target organ, tissue or cell type, compared to a control organ, tissue or cell type. Selective localization resulting in at least a three-fold, four-fold, five-fold, six-fold, seven-fold, eight-fold, nine-fold, ten-fold or higher enrichment in the target organ compared to a control organ, tissue or cell type is more preferred. Alternatively, a phage expressing a targeting peptide sequence that exhibits selective localization preferably shows an increased enrichment in the target organ compared to a control organ when phage recovered from the target organ are reinjected into a second host for another round of screening. Further enrichment may be exhibited following a third round of screening. Another alternative means to determine selective localization is that phage expressing the putative target peptide preferably exhibit a two-fold, more preferably a three-fold or higher enrichment in the target organ compared to control phage that express a non-specific peptide or that have not been genetically engineered to express any putative target peptides. Another means to determine selective localization is that locallization to the target organ of phage expressing the target peptide is at least partially blocked by the co-administration of a synthetic peptide containing the target peptide sequence. "Targeting peptide" and "homing peptide" are used synonymously herein.

A "phage display library" means a collection of phage that have been genetically engineered to express a set of putative targeting peptides on their outer surface. In

preferred embodiments, DNA sequences encoding the putative targeting peptides are inserted in frame into a gene encoding a phage capsule protein. In other preferred embodiments, the putative targeting peptide sequences are in part random mixtures of all twenty amino acids and in part non-random. In certain preferred embodiments the putative targeting peptides of the phage display library exhibit one or more cysteine residues at fixed locations within the targeting peptide sequence.

A "macromolecular complex" refers to a collection of molecules that may be random, ordered or partially ordered in their arrangement. The term encompasses biological organisms such as bacteriophage, viruses, bacteria, unicellular pathogenic organisms, multicellular pathogenic organisms and prokaryotic or eukaryotic cells. The term also encompasses non-living assemblages of molecules, such as liposomes, microcapsules, microparticles, magnetic beads and microdevices. The only requirement is that the complex contains more than one molecule. The molecules may be identical, or may differ from each other.

A "receptor" for a targeting peptide includes but is not limited to any molecule or complex of molecules that binds to a targeting peptide. Non-limiting examples of receptors include peptides, proteins, glycoproteins, lipoproteins, epitopes, lipids, carbohydrates, multi-molecular structures, a specific conformation of one or more molecules and a morphoanatomic entity. In preferred embodiments, a "receptor" is a naturally occurring molecule or complex of molecules that is present on the lumenal surface of cells forming blood vessels within a target organ, tissue or cell type.

A "subject" refers generally to a mammal. In certain preferred embodiments, the subject is a mouse or rabbit. In even more preferred embodiments, the subject is a human.

Phage Display

The methods described herein for identification of targeting peptides involve the *in vivo* administration of phage display libraries. Various methods of phage display and methods for producing diverse populations of peptides are well known in the art. For

example, U.S. Pat. Nos. 5,223,409; 5,622,699 and 6,068,829, each of which is incorporated herein by reference, disclose methods for preparing a phage library. The phage display technique involves genetically manipulating bacteriophage so that small peptides can be expressed on their surface (Smith *et al.*, 1985, 1993). The potential range of applications for this technique is quite broad, and the past decade has seen considerable progress in the construction of phage-displayed peptide libraries and in the development of screening methods in which the libraries are used to isolate peptide ligands. For example, the use of peptide libraries has made it possible to characterize interacting sites and receptor-ligand binding motifs within many proteins, such as antibodies involved in inflammatory reactions or integrins that mediate cellular adherence. This method has also been used to identify novel peptide ligands that serve as leads to the development of peptidomimetic drugs or imaging agents (Arap *et al.*, 1998a). In addition to peptides, larger protein domains such as single-chain antibodies can also be displayed on the surface of phage particles (Arap *et al.*, 1998a).

Targeting amino acid sequences selective for a given organ, tissue or cell type can be isolated by "biopanning" (Pasqualini and Ruoslahti, 1996; Pasqualini, 1999). In brief, a library of phage containing putative targeting peptides is administered to an animal or human and samples of organs, tissues or cell types containing phage are collected. In preferred embodiments utilizing filamentous phage, the phage may be propagated *in vitro* between rounds of biopanning in pilus-positive bacteria. The bacteria are not lysed by the phage but rather secrete multiple copies of phage that display a particular insert. Phage that bind to a target molecule can be eluted from the target organ, tissue or cell type and then amplified by growing them in host bacteria. If desired, the amplified phage can be administered to a host and samples of organs, tissues or cell types again collected. Multiple rounds of biopanning can be performed until a population of selective binders is obtained. The amino acid sequence of the peptides is determined by sequencing the DNA corresponding to the targeting peptide insert in the phage genome. The identified targeting peptide can then be produced as a synthetic peptide by standard protein chemistry techniques (Arap *et al.*, 1998a, Smith *et*

al., 1985). This approach allows circulating targeting peptides to be detected in an unbiased functional assay, without any preconceived notions about the nature of their target. Once a candidate target is identified as the receptor of a targeting peptide, it can be isolated, purified and cloned by using standard biochemical methods (Pasqualini, 1999; Rajotte and Ruoslahti, 1999).

In certain embodiments, a subtraction protocol is used with to further reduce background phage binding. The purpose of subtraction is to remove phage from the library that bind to cells other than the cell of interest, or that bind to inactivated cells. In alternative embodiments, the phage library may be prescreened against a subject who does not possess the targeted cell, tissue or organ. For example, placenta binding peptides may be identified after prescreening a library against a male or non-pregnant female subject After subtraction the library may be screened against the cell, tissue or organ of interest. In another alternative embodiment, an unstimulated, quiescent cell type, tissue or organ may be screened against the library and binding phage removed. The cell line, tissue or organ is then activated, for example by administration of a hormone, growth factor, cytokine or chemokine and the activated cell type, tissue or organ screened against the subtracted phage library.

Other methods of subtraction protocols are known and may be used in the practice of the present invention, for example as disclosed in U.S Patent Nos. 5,840,841, 5,705,610, 5,670,312 and 5,492,807, incorporated herein by reference.

Choice of phage display system.

Previous *in vivo* selection studies performed in mice preferentially employed libraries of random peptides expressed as fusion proteins with the gene III capsule protein in the fUSE5 vector (Pasqualini and Ruoslahti, 1996). The number and diversity of individual clones present in a given library is a significant factor for the success of *in vivo* selection. It is preferred to use primary libraries, which are less likely to have an over-representation of defective phage clones (Koivunen *et al.*, 1999). The preparation of a library should be optimized to between 10^8-10^9 transducing units

(T.U.)/ml. In certain embodiments, a bulk amplification strategy is applied between each round of selection.

Phage libraries displaying linear, cyclic, or double cyclic peptides may be used within the scope of the present invention. However, phage libraries displaying 3 to 10 random residues in a cyclic insert ($CX_{3-10}C$) are preferred, since single cyclic peptides tend to have a higher affinity for the target organ than linear peptides. Libraries displaying double-cyclic peptides (such as CX_3C X_3CX_3C; Rojotte *et al.*, 1998) have been successfully used. However, the production of the cognate synthetic peptides, although possible, can be complex due to the multiple conformers with different dissulfide bridge arrangements .

Identification of homing peptides and receptors by in vivo phage display in mice.

In vivo selection of peptides from phage-display peptide libraries administered to mice has been used to identify targeting peptides selective for normal mouse brain, kidney, lung, skin, pancreas, retina, intestine, uterus, prostate, and adrenal gland (Pasqualini and Ruoslahti, 1996; Pasqualini, 1999; Rajotte *et al.*, 1998). These results show that the vascular endothelium of normal organs is sufficiently heterogenous to allow differential targeting with peptide probes (Pasqualini and Ruoslahti, 1996; Rajotte *et al.*, 1998). A means of identifying peptides that home to the angiogenic vasculature of tumors has been devised, as described below. A panel of peptide motifs that target the blood vessels of tumor xenografts in nude mice has been assembled (Arap *et al.*, 1998a; reviewed in Pasqualini, 1999). These motifs include the sequences RGD-4C, NGR, and GSL. The RGD-4C peptide has previously been identified as selectively binding αv integrins and has been shown to home to the vasculature of tumor xenografts in nude mice (Arap *et al.*, 1998a, 1998b; Pasqualini *et al.*, 1997).

The receptors for the tumor homing RGD4C targeting peptide has been identified as αv integrins (Pasqualini *et al.*, 1997). The αv integrins play an important role in angiogenesis. The αvβ3 and αvβ5 integrins are absent or expressed at low

levels in normal endothelial cells but are induced in angiogenic vasculature of tumors (Brooks *et al.*, 1994; Hammes *et al.*, 1996). Aminopeptidase N/CD13 has recently been identified as an angiogenic receptor for the NGR motif (Burg *et al.*, 1999). Aminopeptidase N/CD13 is strongly expressed not only in the angiogenic blood vessels of prostate cancer in TRAMP mice but also in the normal epithelial prostate tissue.

Tumor-homing phage co-localize with their receptors in the angiogenic vasculature of tumors but not in non-angiogenic blood vessels in normal tissues (Arap *et al.*, 1998b). Immunohistochemical evidence shows that vascular targeting phage bind to human tumor blood vessels in tissue sections (Pasqualini *et al.*, 2000) but not to normal blood vessels. A negative control phage with no insert (fd phage) did not bind to normal or tumor tissue sections. The expression of the angiogenic receptors was evaluated in cell lines, in non-proliferating blood vessels and in activated blood vessels of tumors and other angiogenic tissues such as corpus luteum. Flow cytometry and immunohistochemistry showed that these receptors are expressed in a number of tumor cells and in activated HUVECs (data not shown). The angiogenic receptors were not detected in the vasculature of normal organs of mouseor human tissues.

The distribution of these receptors was analyzed by immunohistochemistry in tumor cells, tumor vasculature, and normal vasculature. Alpha v integrins, CD13, aminopeptidase A, NG2, and MMP-2/MMP-9 - the known receptors in tumor blood vessels - are specifically expressed in angiogenic endothelial cells and pericytes of both human and murine origin. Angiogenic neovasculature expresses markers that are either expressed at very low levels or not at all in non-proliferating endothelial cells (not shown).

The markers of angiogenic endothelium include receptors for vascular growth factors, such as specific subtypes of VEGF and basic FGF receptors, and αv integrins, among many others (Mustonen and Alitalo, 1995). Thus far, identification and isolation of novel molecules characteristic of angiogenic vasculature has been slow, mainly because endothelial cells undergo dramatic phenotypic changes when grown in culture (Watson *et al.*, 1995).

Many of these tumor vascular markers are proteases and some of the markers also serve as viral receptors. Alpha v integrins are receptors for adenoviruses (Wickham *et al.*, 1997c) and CD13 is a receptor for coronaviruses (Look *et al.*, 1989). MMP-2 and MMP-9 are receptors for echoviruses (Koivunen *et al.*, 1999). Aminopeptidase A also appears to be a viral receptor. Bacteriophage may use the same cellular receptors as eukaryotic viruses. These findings suggest that receptors isolated by *in vivo* phage display will have cell internalization capability, a key feature for utilizing the identified peptide motifs as targeted gene therapy carriers.

Targeted delivery

Peptides that home to tumor vasculature have been coupled to cytotoxic drugs or proapoptotic peptides to yield compounds that were more effective and less toxic than the parental compounds in experimental models of mice bearing tumor xenografts (Arap *et al.*, 1998a; Ellerby *et al*, 1999). As described below, the insertion of the RGD-4C peptide into a surface protein of an adenovirus has produced an adenoviral vector that may be used for tumor targeted gene therapy (Arap *et al.*, 1998b).

BRASIL

In preferred embodiments, separation of phage bound to the cells of a target organ, tissue or cell type from unbound phage is achieved using the BRASIL technique (Provisional Patent Application No. 60/231,266 filed September 8, 2000; U.S. Patent Application entitled, "Biopanning and Rapid Analysis of Selective Interactive Ligands (BRASIL)" by Arap, Pasqualini and Giordano, filed concurrently herewith, incorporated herein by reference in its entirety). In BRASIL (Biopanning and Rapid Analysis of Soluble Interactive Ligands), an organ, tissue or cell type is gently separated into cells or small clumps of cells that are suspended in an aqueous phase. The aqueous phase is layered over an organic phase of appropriate density and centrifuged. Cells attached to bound phage are pelleted at the bottom of the centrifuge tube, while unbound phage remain in the aqueous phase. This allows a more efficient separation of bound from unbound phage, while maintaining the binding interaction between phage

and cell. BRASIL may be performed in an *in vivo* protocol, in which organs, tissues or cell types are exposed to a phage display library by intravenous administration, or by an *ex vivo* protocol, where the cells are exposed to the phage library in the aqueous phase before centrifugation.

Proteins and Peptides

In certain embodiments, the present invention concerns novel compositions comprising at least one protein or peptide. As used herein, a protein or peptide generally refers, but is not limited to, a protein of greater than about 200 amino acids, up to a full length sequence translated from a gene; a polypeptide of greater than about 100 amino acids; and/or a peptide of from about 3 to about 100 amino acids. For convenience, the terms "protein," "polypeptide" and "peptide are used interchangeably herein.

In certain embodiments the size of the at least one protein or peptide may comprise, but is not limited to, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, about 110, about 120, aboout 130, about 140, about 150, about 160, about 170, about 180, about 190, about 200, about 210, about 220, about 230, about 240, about 250, about 275, about 300, about 325, about 350, about 375, about 400, about 425, about 450, about 475, about 500, about 525, about 550, about 575, about 600, about 625, about 650, about 675, about 700, about 725, about 750, about 775, about 800, about 825, about 850, about 875, about 900, about 925, about 950, about 975, about 1000, about 1100, about 1200, about 1300, about 1400, about 1500, about 1750, about 2000, about 2250, about 2500 or greater amino acid residues.

As used herein, an "amino acid residue" refers to any naturally occuring amino acid, any amino acid derivitive or any amino acid mimic known in the art. In certain embodiments, the residues of the protein or peptide are sequential, without any non-amino acid interrupting the sequence of amino acid residues. In other embodiments, the sequence may comprise one or more non-amino acid moieties. In particular embodiments, the sequence of residues of the protein or peptide may be interrupted by one or more non-amino acid moieties.

Accordingly, the term "protein or peptide" encompasses amino acid sequences comprising at least one of the 20 common amino acids found in naturally occurring proteins, or at least one modified or unusual amino acid, including but not limited to those shown on Table 1 below.

TABLE 1

Modified and Unusual Amino Acids

Abbr.	Amino Acid	Abbr.	Amino Acid
Aad	2-Aminoadipic acid	EtAsn	N-Ethylasparagine
Baad	3- Aminoadipic acid	Hyl	Hydroxylysine
Bala	β-alanine, β-Amino-propionic acid	AHyl	allo-Hydroxylysine
Abu	2-Aminobutyric acid	3Hyp	3-Hydroxyproline
4Abu	4- Aminobutyric acid, piperidinic acid	4Hyp	4-Hydroxyproline
Acp	6-Aminocaproic acid	Ide	Isodesmosine
Ahe	2-Aminoheptanoic acid	AIle	allo-Isoleucine
Aib	2-Aminoisobutyric acid	MeGly	N-Methylglycine, sarcosine
Baib	3-Aminoisobutyric acid	MeIle	N-Methylisoleucine
Apm	2-Aminopimelic acid	MeLys	6-N-Methyllysine
Dbu	2,4-Diaminobutyric acid	MeVal	N-Methylvaline
Des	Desmosine	Nva	Norvaline
Dpm	2,2'-Diaminopimelic acid	Nle	Norleucine
Dpr	2,3-Diaminopropionic acid	Orn	Ornithine

TABLE 1 Modified and Unusual Amino Acids			
Abbr.	Amino Acid	Abbr.	Amino Acid
EtGly	N-Ethylglycine		

Proteins or peptides may be made by any technique known to those of skill in the art, including the expression of proteins, polypeptides or peptides through standard molecular biological techniques, the isolation of proteins or peptides from natural sources, or the chemical synthesis of proteins or peptides. The nucleotide and protein, polypeptide and peptide sequences corresponding to various genes have been previously disclosed, and may be found at computerized databases known to those of ordinary skill in the art. One such database is the National Center for Biotechnology Information's Genbank and GenPept databases (http://www.ncbi.nlm.nih.gov/). The coding regions for known genes may be amplified and/or expressed using the techniques disclosed herein or as would be know to those of ordinary skill in the art. Alternatively, various commercial preparations of proteins, polypeptides and peptides are known to those of skill in the art.

Peptide mimetics

Another embodiment for the preparation of polypeptides according to the invention is the use of peptide mimetics. Mimetics are peptide-containing molecules that mimic elements of protein secondary structure. See, for example, Johnson *et al.*, "Peptide Turn Mimetics" in *BIOTECHNOLOGY AND PHARMACY*, Pezzuto *et al.*, Eds., Chapman and Hall, New York (1993), incorporated herein by reference. The underlying rationale behind the use of peptide mimetics is that the peptide backbone of proteins exists chiefly to orient amino acid side chains in such a way as to facilitate molecular interactions, such as those of antibody and antigen. A peptide mimetic is expected to permit molecular interactions similar to the natural molecule. These principles may be used to engineer second generation molecules having many of the

natural properties of the targeting peptides disclosed herein, but with altered and even improved characteristics.

Fusion proteins

Other embodiments of the present invention concern fusion proteins. These molecules generally have all or a substantial portion of a targeting peptide, linked at the N- or C-terminus, to all or a portion of a second polypeptide or proteion. For example, fusions may employ leader sequences from other species to permit the recombinant expression of a protein in a heterologous host. Another useful fusion includes the addition of an immunologically active domain, such as an antibody epitope, to facilitate purification of the fusion protein. Inclusion of a cleavage site at or near the fusion junction will facilitate removal of the extraneous polypeptide after purification. Other useful fusions include linking of functional domains, such as active sites from enzymes, glycosylation domains, cellular targeting signals or transmembrane regions. In preferred embodiments, the fusion proteins of the instant invention comprise a targeting peptide linked to a therapeutic protein or peptide. Examples of proteins or peptides that may be incorporated into a fusion protein include cytostatic proteins, cytocidal proteins, pro-apoptosis agents, anti-angiogenic agents, hormones, cytokines, growth factors, peptide drugs, antibodies, Fab fragments antibodies, antigens, receptor proteins, enzymes, lectins, MHC proteins, cell adhesion proteins and binding proteins. These examples are not meant to be limiting and it is contemplated that within the scope of the present invention virtually and protein or peptide could be incorporated into a fusion protein comprising a targeting peptide. Methods of generating fusion proteins are well known to those of skill in the art. Such proteins can be produced, for example, by chemical attachment using bifunctional cross-linking reagents, by *de novo* synthesis of the complete fusion protein, or by attachment of a DNA sequence encoding the targeting peptide to a DNA sequence encoding the second peptide or protein, followed by expression of the intact fusion protein.

Protein purification

In certain embodiments a protein or peptide may be isolated or purified. Protein purification techniques are well known to those of skill in the art. These techniques involve, at one level, the homogenization and crude fractionation of the cells, tissue or organ to polypeptide and non-polypeptide fractions. The protein or polypeptide of interest may be further purified using chromatographic and electrophoretic techniques to achieve partial or complete purification (or purification to homogeneity). Analytical methods particularly suited to the preparation of a pure peptide are ion-exchange chromatography, gel exclusion chromatography, polyacrylamide gel electrophoresis, affinity chromatography, immunoaffinity chromatography and isoelectric focusing. An example of receptor protein purification by affinity chromatography is disclosed in U.S. Patent No. 5,206,347, the entire text of which is incorporated herein by reference. A particularly efficient method of purifying peptides is fast protein liquid chromatography (FPLC) or even HPLC.

A purified protein or peptide is intended to refer to a composition, isolatable from other components, wherein the protein or peptide is purified to any degree relative to its naturally-obtainable state. An isolated or purified protein or peptide, therefore, also refers to a protein or peptide free from the environment in which it may naturally occur. Generally, "purified" will refer to a protein or peptide composition that has been subjected to fractionation to remove various other components, and which composition substantially retains its expressed biological activity. Where the term "substantially purified" is used, this designation will refer to a composition in which the protein or peptide forms the major component of the composition, such as constituting about 50%, about 60%, about 70%, about 80%, about 90%, about 95%, or more of the proteins in the composition.

Various methods for quantifying the degree of purification of the protein or peptide are known to those of skill in the art in light of the present disclosure. These include, for example, determining the specific activity of an active fraction, or assessing the amount of polypeptides within a fraction by SDS/PAGE analysis. A preferred

method for assessing the purity of a fraction is to calculate the specific activity of the fraction, to compare it to the specific activity of the initial extract, and to thus calculate the degree of purity therein, assessed by a "-fold purification number." The actual units used to represent the amount of activity will, of course, be dependent upon the particular assay technique chosen to follow the purification, and whether or not the expressed protein or peptide exhibits a detectable activity.

Various techniques suitable for use in protein purification are well known to those of skill in the art. These include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like, or by heat denaturation, followed by: centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combinations of these and other techniques. As is generally known in the art, it is believed that the order of conducting the various purification steps may be changed, or that certain steps may be omitted, and still result in a suitable method for the preparation of a substantially purified protein or peptide.

There is no general requirement that the protein or peptide always be provided in their most purified state. Indeed, it is contemplated that less substantially purified products will have utility in certain embodiments. Partial purification may be accomplished by using fewer purification steps in combination, or by utilizing different forms of the same general purification scheme. For example, it is appreciated that a cation-exchange column chromatography performed utilizing an HPLC apparatus will generally result in a greater "-fold" purification than the same technique utilizing a low pressure chromatography system. Methods exhibiting a lower degree of relative purification may have advantages in total recovery of protein product, or in maintaining the activity of an expressed protein.

Affinity chromatography is a chromatographic procedure that relies on the specific affinity between a substance to be isolated and a molecule to which it can specifically bind to. This is a receptor-ligand type of interaction. The column material

is synthesized by covalently coupling one of the binding partners to an insoluble matrix. The column material is then able to specifically adsorb the substance from the solution. Elution occurs by changing the conditions to those in which binding will not occur (*e.g.*, altered pH, ionic strength, temperature, *etc.*). The matrix should be a substance that itself does not adsorb molecules to any significant extent and that has a broad range of chemical, physical and thermal stability. The ligand should be coupled in such a way as to not affect its binding properties. The ligand should also provide relatively tight binding. And it should be possible to elute the substance without destroying the sample or the ligand.

Synthetic Peptides

Because of their relatively small size, the targeting peptides of the invention can be synthesized in solution or on a solid support in accordance with conventional techniques. Various automatic synthesizers are commercially available and can be used in accordance with known protocols. See, for example, Stewart and Young, (1984); Tam *et al.*, (1983); Merrifield, (1986); and Barany and Merrifield (1979), each incorporated herein by reference. Short peptide sequences, usually from about 6 up to about 35 to 50 amino acids, can be readily synthesized by such methods. Alternatively, recombinant DNA technology may be employed wherein a nucleotide sequence which encodes a peptide of the invention is inserted into an expression vector, transformed or transfected into an appropriate host cell, and cultivated under conditions suitable for expression.

Antibodies

In certain embodiments, it may be desirable to make antibodies against the identified targeting peptides or their receptors. The appropriate targeting peptide or receptor, or portions thereof, may be coupled, bonded, bound, conjugated, or chemically-linked to one or more agents via linkers, polylinkers, or derivatized amino acids. This may be performed such that a bispecific or multivalent composition or vaccine is produced. It is further envisioned that the methods used in the preparation of

these compositions are familiar to those of skill in the art and should be suitable for administration to humans, *i.e.*, pharmaceutically acceptable. Preferred agents are the carriers are keyhole limpet hemocyanin (KLH) or bovine serum albumin (BSA).

The term "antibody" is used to refer to any antibody-like molecule that has an antigen binding region, and includes antibody fragments such as Fab', Fab, $F(ab')_2$, single domain antibodies (DABs), Fv, scFv (single chain Fv), and the like. Techniques for preparing and using various antibody-based constructs and fragments are well known in the art. Means for preparing and characterizing antibodies are also well known in the art (See, *e.g.*, Antibodies: A Laboratory Manual, Cold Spring Harbor Laboratory, 1988; incorporated herein by reference).

Cytokines and chemokines

In certain embodiments, it may be desirable to couple specific bioactive agents to one or more targeting peptides for targeted delivery to an organ, tissue or cell type. Such agents include, but are not limited to, cytokines, chemikines, pro-apoptosis factors and anti-angiogenic factors. The term "cytokine" is a generic term for proteins released by one cell population which act on another cell as intercellular mediators. Examples of such cytokines are lymphokines, monokines, growth factors and traditional polypeptide hormones. Included among the cytokines are growth hormones such as human growth hormone, N-methionyl human growth hormone, and bovine growth hormone; parathyroid hormone; thyroxine; insulin; proinsulin; relaxin; prorelaxin; glycoprotein hormones such as follicle stimulating hormone (FSH), thyroid stimulating hormone (TSH), and luteinizing hormone (LH); hepatic growth factor; prostaglandin, fibroblast growth factor; prolactin; placental lactogen, OB protein; tumor necrosis factor-.alpha. and -.beta.; mullerian-inhibiting substance; mouse gonadotropin-associated peptide; inhibin; activin; vascular endothelial growth factor; integrin; thrombopoietin (TPO); nerve growth factors such as NGF-.beta.; platelet-growth factor; transforming growth factors (TGFs) such as TGF-.alpha. and TGF-.beta.; insulin-like growth factor-I and -II; erythropoietin (EPO); osteoinductive factors; interferons such as interferon-α, -.β, and -γ; colony stimulating factors (CSFs) such as macrophage-CSF (M-CSF); granulocyte-

macrophage-CSF (GM-CSF); and granulocyte-CSF (G-CSF); interleukins (ILs) such as IL-1, IL-1.alpha., IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12; IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, LIF, G-CSF, GM-CSF, M- CSF, EPO, kit-ligand or FLT-3, angiostatin, thrombospondin, endostatin, tumor necrosis factor and LT. As used herein, the term cytokine includes proteins from natural sources or from recombinant cell culture and biologically active equivalents of the native sequence cytokines.

Chemokines generally act as chemoattractants to recruit immune effector cells to the site of chemokine expression. It may be advantageous to express a particular chemokine gene in combination with, for example, a cytokine gene, to enhance the recruitment of other immune system components to the site of treatment. Chemokines include, but are not limited to, RANTES, MCAF, MIP1-alpha, MIP1-Beta, and IP-10. The skilled artisan will recognize that certain cytokines are also known to have chemoattractant effects and could also be classified under the term chemokines.

Imaging agents and radioisotopes

In certain embodiments, the claimed peptides or proteins of the present invention may be attached to imaging agents of use for imaging and diagnosis of various diseased organs, tissues or cell types. Many appropriate imaging agents are known in the art, as are methods for their attachment to proteins or peptides (see, *e.g.*, U.S. patents 5,021,236 and 4,472,509, both incorporated herein by reference). Certain attachment methods involve the use of a metal chelate complex employing, for example, an organic chelating agent such a DTPA attached to the protein or peptide (U.S. Patent 4,472,509). Proteins or peptides also may be reacted with an enzyme in the presence of a coupling agent such as glutaraldehyde or periodate. Conjugates with fluorescein markers are prepared in the presence of these coupling agents or by reaction with an isothiocyanate.

Non-limiting examples of paramagnetic ions of potential use as imaging agents include chromium (III), manganese (II), iron (III), iron (II), cobalt (II), nickel (II),

copper (II), neodymium (III), samarium (III), ytterbium (III), gadolinium (III), vanadium (II), terbium (III), dysprosium (III), holmium (III) and erbium (III), with gadolinium being particularly preferred. Ions useful in other contexts, such as X-ray imaging, include but are not limited to lanthanum (III), gold (III), lead (II), and especially bismuth (III).

Radioisotopes of potential use as imaging or therapeutic agents include astatine^{211}, ^{14}carbon, ^{51}chromium, ^{36}chlorine, ^{57}cobalt, ^{58}cobalt, copper^{67}, ^{152}Eu, gallium^{67}, ^{3}hydrogen, iodine^{123}, iodine^{125}, iodine^{131}, indium^{111}, ^{59}iron, ^{32}phosphorus, rhenium^{186}, rhenium^{188}, ^{75}selenium, ^{35}sulphur, technicium^{99m} and yttrium^{90}. ^{125}I is often being preferred for use in certain embodiments, and technicium^{99m} and indium^{111} are also often preferred due to their low energy and suitability for long range detection.

Radioactively labeled proteins or peptides of the present invention may be produced according to well-known methods in the art. For instance, they can be iodinated by contact with sodium or potassium iodide and a chemical oxidizing agent such as sodium hypochlorite, or an enzymatic oxidizing agent, such as lactoperoxidase. Proteins or peptides according to the invention may be labeled with technetium-^{99m} by ligand exchange process, for example, by reducing pertechnate with stannous solution, chelating the reduced technetium onto a Sephadex column and applying the peptide to this column or by direct labeling techniques, *e.g.*, by incubating pertechnate, a reducing agent such as $SNCl_2$, a buffer solution such as sodium-potassium phthalate solution, and the peptide. Intermediary functional groups which are often used to bind radioisotopes which exist as metallic ions to peptides are diethylenetriaminepentaacetic acid (DTPA) and ethylene diaminetetracetic acid (EDTA). Also contemplated for use are fluorescent labels, including rhodamine, fluorescein isothiocyanate and renographin.

In certain embodiments, the claimed proteins or peptides may be linked to a secondary binding ligand or to an enzyme (an enzyme tag) that will generate a colored product upon contact with a chromogenic substrate. Examples of suitable enzymes include urease, alkaline phosphatase, (horseradish) hydrogen peroxidase and glucose

oxidase. Preferred secondary binding ligands are biotin and avidin or streptavidin compounds. The use of such labels is well known to those of skill in the art in light and is described, for example, in U.S. Patents 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241; each incorporated herein by reference.

Cross-linkers

Bifunctional cross-linking reagents have been extensively used for a variety of purposes including preparation of affinity matrices, modification and stabilization of diverse structures, identification of ligand and receptor binding sites, and structural studies. Homobifunctional reagents that carry two identical functional groups proved to be highly efficient in inducing cross-linking between identical and different macromolecules or subunits of a macromolecule, and linking of polypeptide ligands to their specific binding sites. Heterobifunctional reagents contain two different functional groups. By taking advantage of the differential reactivities of the two different functional groups, cross-linking can be controlled both selectively and sequentially. The bifunctional cross-linking reagents can be divided according to the specificity of their functional groups, *e.g.,* amino, sulfhydryl, guanidino, indole, carboxyl specific groups. Of these, reagents directed to free amino groups have become especially popular because of their commercial availability, ease of synthesis and the mild reaction conditions under which they can be applied. A majority of heterobifunctional cross-linking reagents contains a primary amine-reactive group and a thiol-reactive group.

Exemplary methods for cross-linking ligands to liposomes are described in U.S. Patent 5,603,872 and U.S. Patent 5,401,511, each specifically incorporated herein by reference in its entirety). Various ligands can be covalently bound to liposomal surfaces through the cross-linking of amine residues. Liposomes, in particular, multilamellar vesicles (MLV) or unilamellar vesicles such as microemulsified liposomes (MEL) and large unilamellar liposomes (LUVET), each containing phosphatidylethanolamine (PE), have been prepared by established procedures. The inclusion of PE in the liposome provides an active functional residue, a primary amine,

on the liposomal surface for cross-linking purposes. Ligands such as epidermal growth factor (EGF) have been successfully linked with PE-liposomes. Ligands are bound covalently to discrete sites on the liposome surfaces. The number and surface density of these sites are dictated by the liposome formulation and the liposome type. The liposomal surfaces may also have sites for non-covalent association. To form covalent conjugates of ligands and liposomes, cross-linking reagents have been studied for effectiveness and biocompatibility. Cross-linking reagents include glutaraldehyde (GAD), bifunctional oxirane (OXR), ethylene glycol diglycidyl ether (EGDE), and a water soluble carbodiimide, preferably 1-ethyl-3-(3-dimethylaminopropyl) carbodiimide (EDC). Through the complex chemistry of cross-linking, linkage of the amine residues of the recognizing substance and liposomes is established.

In another example, heterobifunctional cross-linking reagents and methods of using the cross-linking reagents are described (U.S. Patent 5,889,155, specifically incorporated herein by reference in its entirety). The cross-linking reagents combine a nucleophilic hydrazide residue with an electrophilic maleimide residue, allowing coupling in one example, of aldehydes to free thiols. The cross-linking reagent can be modified to cross-link various functional groups.

Nucleic Acids

Nucleic acids according to the present invention may encode a targeting peptide, a receptor protein or a fusion protein. The nucleic acid may be derived from genomic DNA, complementary DNA (cDNA) or synthetic DNA. Where incorporation into an expression vector is desired, the nucleic acid may also comprise a natural intron or an intron derived from another gene. Such engineered molecules are sometime referred to as "mini-genes."

A "nucleic acid" as used herein includes single-stranded and double-stranded molecules, as well as DNA, RNA, chemically modified nucleic acids and nucleic acid analogs. It is contemplated that a nucleic acid within the scope of the present invention may be of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25,

26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, about 110, about 120, aboout 130, about 140, about 150, about 160, about 170, about 180, about 190, about 200, about 210, about 220, about 230, about 240, about 250, about 275, about 300, about 325, about 350, about 375, about 400, about 425, about 450, about 475, about 500, about 525, about 550, about 575, about 600, about 625, about 650, about 675, about 700, about 725, about 750, about 775, about 800, about 825, about 850, about 875, about 900, about 925, about 950, about 975, about 1000, about 1100, about 1200, about 1300, about 1400, about 1500, about 1750, about 2000, about 2250, about 2500 or greater nucleotide residues in length.

It is contemplated that targeting peptides, fusion proteins and receptors may be encoded by any nucleic acid sequence that encodes the appropriate amino acid sequence. The design and production of nucleic acids encoding a desired amino acid sequence is well known to those of skill in the art, using standardized codon tables (see Table 2 below). In preferred embodiments, the codons selected for encoding each amino acid may be modified to optimize expression of the nucleic acid in the host cell of interest. Codon preferences for various species of host cell are well known in the art.

TABLE 2

Amino Acid			**Codons**
Alanine	Ala	A	GCA GCC GCG GCU
Cysteine	Cys	C	UGC UGU
Aspartic acid	Asp	D	GAC GAU
Glutamic acid	Glu	E	GAA GAG
Phenylalanine	Phe	F	UUC UUU
Glycine	Gly	G	GGA GGC GGG GGU

Histidine	His	H	CAC CAU
Isoleucine	Ile	I	AUA AUC AUU
Lysine	Lys	K	AAA AAG
Leucine	Leu	L	UUA UUG CUA CUC CUG CUU
Methionine	Met	M	AUG
Asparagine	Asn	N	AAC AAU
Proline	Pro	P	CCA CCC CCG CCU
Glutamine	Gln	Q	CAA CAG
Arginine	Arg	R	AGA AGG CGA CGC CGG CGU
Serine	Ser	S	AGC AGU UCA UCC UCG UCU
Threonine	Thr	T	ACA ACC ACG ACU
Valine	Val	V	GUA GUC GUG GUU
Tryptophan	Trp	W	UGG
Tyrosine	Tyr	Y	UAC UAU

In addition to nucleic acids encoding the desired targeting peptide, fusion protein or receptor amino acid sequence, the present invention encompasses complementary nucleic acids that hybridize under high stringency conditions with such coding nucleic acid sequences. High stringency conditions for nucleic acid hybridization are well known in the art. For example, conditions may comprise low salt and/or high temperature conditions, such as provided by about 0.02 M to about 0.15 M NaCl at temperatures of about 50°C to about 70°C. It is understood that the temperature and ionic strength of a desired stringency are determined in part by the length of the particular nucleic acid(s), the length and nucleotide content of the target sequence(s), the charge composition of the nucleic acid(s), and to the presence or concentration of formamide, tetramethylammonium chloride or other solvent(s) in a hybridization mixture.

Vectors for Cloning, Gene Transfer and Expression

In certain embodiments expression vectors are employed to express the targeting peptide or fusion protein, which can then be purified and used. In other embodiments, the expression vectors are used in gene therapy. Expression requires that appropriate signals be provided in the vectors, and which include various regulatory elements, such as enhancers/promoters from both viral and mammalian sources that drive expression of the genes of interest in host cells. Elements designed to optimize messenger RNA stability and translatability in host cells also are known.

Regulatory Elements

The terms "expression construct" or "expression vector" are meant to include any type of genetic construct containing a nucleic acid coding for a gene product in which part or all of the nucleic acid coding sequence is capable of being transcribed. In preferred embodiments, the nucleic acid encoding a gene product is under transcriptional control of a promoter. A "promoter" refers to a DNA sequence recognized by the synthetic machinery of the cell, or introduced synthetic machinery, required to initiate the specific transcription of a gene. The phrase "under transcriptional control" means that the promoter is in the correct location and orientation in relation to the nucleic acid to control RNA polymerase initiation and expression of the gene.

The particular promoter employed to control the expression of a nucleic acid sequence of interest is not believed to be important, so long as it is capable of directing the expression of the nucleic acid in the targeted cell. Thus, where a human cell is targeted, it is preferable to position the nucleic acid coding region adjacent and under the control of a promoter that is capable of being expressed in a human cell. Generally speaking, such a promoter might include either a human or viral promoter.

In various embodiments, the human cytomegalovirus (CMV) immediate early gene promoter, the SV40 early promoter, the Rous sarcoma virus long terminal repeat, rat insulin promoter, and glyceraldehyde-3-phosphate dehydrogenase promoter can be

used to obtain high-level expression of the coding sequence of interest. The use of other viral or mammalian cellular or bacterial phage promoters which are well-known in the art to achieve expression of a coding sequence of interest is contemplated as well, provided that the levels of expression are sufficient for a given purpose.

Where a cDNA insert is employed, typically one will typically include a polyadenylation signal to effect proper polyadenylation of the gene transcript. The nature of the polyadenylation signal is not believed to be crucial to the successful practice of the invention, and any such sequence may be employed, such as human growth hormone and SV40 polyadenylation signals. Also contemplated as an element of the expression construct is a terminator. These elements can serve to enhance message levels and to minimize read through from the construct into other sequences.

Selectable Markers

In certain embodiments of the invention, the cells containing nucleic acid constructs of the present invention may be identified *in vitro* or *in vivo* by including a marker in the expression construct. Such markers would confer an identifiable change to the cell permitting easy identification of cells containing the expression construct. Usually the inclusion of a drug selection marker aids in cloning and in the selection of transformants. For example, genes that confer resistance to neomycin, puromycin, hygromycin, DHFR, GPT, zeocin, and histidinol are useful selectable markers. Alternatively, enzymes such as herpes simplex virus thymidine kinase (*tk*) or chloramphenicol acetyltransferase (CAT) may be employed. Immunologic markers also can be employed. The selectable marker employed is not believed to be important, so long as it is capable of being expressed simultaneously with the nucleic acid encoding a gene product. Further examples of selectable markers are well known to one of skill in the art.

Delivery of Expression Vectors

There are a number of ways in which expression vectors may introduced into cells. In certain embodiments of the invention, the expression construct comprises a

virus or engineered construct derived from a viral genome. The ability of certain viruses to enter cells via receptor-mediated endocytosis, to integrate into host cell genome, and express viral genes stably and efficiently have made them attractive candidates for the transfer of foreign genes into mammalian cells (Ridgeway, 1988; Nicolas and Rubenstein, 1988; Baichwal and Sugden, 1986; Temin, 1986). Preferred gene therapy vectors are generally viral vectors.

Although some viruses that can accept foreign genetic material are limited in the number of nucleotides they can accommodate and in the range of cells they infect, these viruses have been demonstrated to successfully effect gene expression. However, adenoviruses do not integrate their genetic material into the host genome and therefore do not require host replication for gene expression making them ideally suited for rapid, efficient, heterologous gene expression. Techniques for preeparing replication infective viruses are well known in the art.

In using viral delivery systems, one will desire to purify the virion sufficiently to render it essentially free of undesirable contaminants, such as defective interfering viral particles or endotoxins and other pyrogens such that it will not cause any untoward reactions in the cell, animal or individual receiving the vector construct. A preferred means of purifying the vector involves the use of buoyant density gradients, such as cesium chloride gradient centrifugation.

DNA viruses used as gene vectors include the papovaviruses (*e.g.*, simian virus 40, bovine papilloma virus, and polyoma) (Ridgeway, 1988; Baichwal and Sugden, 1986) and adenoviruses (Ridgeway, 1988; Baichwal and Sugden, 1986).

One of the preferred methods for *in vivo* delivery involves the use of an adenovirus expression vector. Although adenovirus vectors are known to have a low capacity for integration into genomic DNA, this feature is counterbalanced by the high efficiency of gene transfer afforded by these vectors. "Adenovirus expression vector" is meant to include, but is not limited to, constructs containing adenovirus sequences

sufficient to (a) support packaging of the construct and (b) to express an antisense or a sense polynucleotide that has been cloned therein.

The expression vector comprises a genetically engineered form of adenovirus. Knowledge of the genetic organization of adenovirus, a 36 kb, linear, double-stranded DNA virus, allows substitution of large pieces of adenoviral DNA with foreign sequences up to 7 kb (Grunhaus and Horwitz, 1992). In contrast to retroviral infection, the adenoviral infection of host cells does not result in chromosomal integration because adenoviral DNA can replicate in an episomal manner without potential genotoxicity. Also, adenoviruses are structurally stable, and no genome rearrangement has been detected after extensive amplification. Adenovirus can infect virtually all epithelial cells regardless of their cell cycle stage. So far, adenoviral infection appears to be linked only to mild disease such as acute respiratory disease in humans.

Adenovirus is particularly suitable for use as a gene transfer vector because of its mid-sized genome, ease of manipulation, high titer, wide target cell range and high infectivity. Both ends of the viral genome contain 100-200 base pair inverted repeats (ITRs), which are *cis* elements necessary for viral DNA replication and packaging. The early (E) and late (L) regions of the genome contain different transcription units that are divided by the onset of viral DNA replication. The E1 region (E1A and E1B) encodes proteins responsible for the regulation of transcription of the viral genome and a few cellular genes. The expression of the E2 region (E2A and E2B) results in the synthesis of the proteins for viral DNA replication. These proteins are involved in DNA replication, late gene expression and host cell shut-off (Renan, 1990). The products of the late genes, including the majority of the viral capsid proteins, are expressed only after significant processing of a single primary transcript issued by the major late promoter (MLP). The MLP, (located at 16.8 m.u.) is particularly efficient during the late phase of infection, and all the mRNAs issued from this promoter possess a 5′-tripartite leader (TPL) sequence which makes them preferred mRNAs for translation.

In currently used systems, recombinant adenovirus is generated from homologous recombination between shuttle vector and provirus vector. Due to the possible recombination between two proviral vectors, wild-type adenovirus may be generated from this process. Therefore, it is critical to isolate a single clone of virus from an individual plaque and examine its genomic structure.

Generation and propagation of adenovirus vectors which are replication deficient depend on a unique helper cell line, designated 293, which is transformed from human embryonic kidney cells by Ad5 DNA fragments and constitutively expresses E1 proteins (Graham *et al.*, 1977). Since the E3 region is dispensable from the adenovirus genome (Jones and Shenk, 1978), the current adenovirus vectors, with the help of 293 cells, carry foreign DNA in either the E1, the E3, or both regions (Graham and Prevec, 1991). In nature, adenovirus can package approximately 105% of the wild-type genome (Ghosh-Choudhury *et al.*, 1987), providing capacity for about 2 extra kb of DNA. Combined with the approximately 5.5 kb of DNA that is replaceable in the E1 and E3 regions, the maximum capacity of the current adenovirus vector is under 7.5 kb, or about 15% of the total length of the vector. More than 80% of the adenovirus viral genome remains in the vector backbone and is the source of vector-borne cytotoxicity. Also, the replication deficiency of the E1-deleted virus is incomplete. For example, leakage of viral gene expression has been observed with the currently available vectors at high multiplicities of infection (MOI) (Mulligan, 1993).

Helper cell lines may be derived from human cells such as human embryonic kidney cells, muscle cells, hematopoietic cells or other human embryonic mesenchymal or epithelial cells. Alternatively, the helper cells may be derived from the cells of other mammalian species that are permissive for human adenovirus. Such cells include, *e.g.*, Vero cells or other monkey embryonic mesenchymal or epithelial cells. As discussed, the preferred helper cell line is 293.

Racher *et al.*, (1995) disclosed improved methods for culturing 293 cells and propagating adenovirus. In one format, natural cell aggregates are grown by inoculating

individual cells into 1 liter siliconized spinner flasks (Techne, Cambridge, UK) containing 100-200 ml of medium. Following stirring at 40 rpm, the cell viability is estimated with trypan blue. In another format, Fibra-Cel microcarriers (Bibby Sterlin, Stone, UK) (5 g/l) are employed as follows. A cell innoculum, resuspended in 5 ml of medium, is added to the carrier (50 ml) in a 250 ml Erlenmeyer flask and left stationary, with occasional agitation, for 1 to 4 h. The medium is then replaced with 50 ml of fresh medium and shaking is initiated. For virus production, cells are allowed to grow to about 80% confluence, after which time the medium is replaced (to 25% of the final volume) and adenovirus added at an MOI of 0.05. Cultures are left stationary overnight, following which the volume is increased to 100% and shaking is commenced for another 72 hr.

Other than the requirement that the adenovirus vector be replication defective, or at least conditionally defective, the nature of the adenovirus vector is not believed to be crucial to the successful practice of the invention. The adenovirus may be of any of the 42 different known serotypes or subgroups A-F. Adenovirus type 5 of subgroup C is the preferred starting material in order to obtain the conditional replication-defective adenovirus vector for use in the present invention. This is because Adenovirus type 5 is a human adenovirus about which a great deal of biochemical and genetic information is known, and it has historically been used for most constructions employing adenovirus as a vector.

A typical vector applicable to practicing the present invention is replication defective and will not have an adenovirus E1 region. Thus, it are most convenient to introduce the polynucleotide encoding the gene at the position from which the E1-coding sequences have been removed. However, the position of insertion of the construct within the adenovirus sequences is not critical. The polynucleotide encoding the gene of interest may also be inserted in lieu of the deleted E3 region in E3 replacement vectors as described by Karlsson *et al.*, (1986) or in the E4 region where a helper cell line or helper virus complements the E4 defect.

Adenovirus is easy to grow and manipulate and exhibits broad host range *in vitro* and *in vivo*. This group of viruses can be obtained in high titers, *e.g.*, 10^9-10^{11} plaque-forming units per ml, and they are highly infective. The life cycle of adenovirus does not require integration into the host cell genome. The foreign genes delivered by adenovirus vectors are episomal and, therefore, have low genotoxicity to host cells. No side effects have been reported in studies of vaccination with wild-type adenovirus (Couch *et al.*, 1963; Top *et al.*, 1971), demonstrating their safety and therapeutic potential as *in vivo* gene transfer vectors.

Adenovirus vectors have been used in eukaryotic gene expression (Levrero *et al.*, 1991; Gomez-Foix *et al.*, 1992) and vaccine development (Grunhaus and Horwitz, 1992; Graham and Prevec, 1991). Animal studies have suggested that recombinant adenovirus could be used for gene therapy (Stratford-Perricaudet and Perricaudet, 1991; Stratford-Perricaudet *et al.*, 1990; Rich *et al.*, 1993). Studies in administering recombinant adenovirus to different tissues include trachea instillation (Rosenfeld *et al.*, 1991; Rosenfeld *et al.*, 1992), muscle injection (Ragot *et al.*, 1993), peripheral intravenous injections (Herz and Gerard, 1993) and stereotactic innoculation into the brain (Le Gal La Salle *et al.*, 1993).

Other gene transfer vectors may be constructed from retroviruses. The retroviruses are a group of single-stranded RNA viruses characterized by an ability to convert their RNA to double-stranded DNA in infected cells by a process of reverse-transcription (Coffin, 1990). The resulting DNA then stably integrates into cellular chromosomes as a provirus and directs synthesis of viral proteins. The integration results in the retention of the viral gene sequences in the recipient cell and its descendants. The retroviral genome contains three genes, *gag*, *pol*, and *env*. that code for capsid proteins, polymerase enzyme, and envelope components, respectively. A sequence found upstream from the *gag* gene contains a signal for packaging of the genome into virions. Two long terminal repeat (LTR) sequences are present at the 5′ and 3′ ends of the viral genome. These contain strong promoter and enhancer sequences, and also are required for integration in the host cell genome (Coffin, 1990).

In order to construct a retroviral vector, a nucleic acid encoding protein of interest is inserted into the viral genome in the place of certain viral sequences to produce a virus that is replication-defective. In order to produce virions, a packaging cell line containing the *gag, pol,* and *env* genes, but without the LTR and packaging components, is constructed (Mann *et al.,* 1983). When a recombinant plasmid containing a cDNA, together with the retroviral LTR and packaging sequences is introduced into this cell line (by calcium phosphate precipitation for example), the packaging sequence allows the RNA transcript of the recombinant plasmid to be packaged into viral particles, which are then secreted into the culture media (Nicolas and Rubenstein, 1988; Temin, 1986; Mann *et al.,* 1983). The media containing the recombinant retroviruses is then collected, optionally concentrated, and used for gene transfer. Retroviral vectors are capable of infecting a broad variety of cell types. However, integration and stable expression require the division of host cells (Paskind *et al.,* 1975).

There are certain limitations to the use of retrovirus vectors. For example, retrovirus vectors usually integrate into random sites in the cell genome. This can lead to insertional mutagenesis through the interruption of host genes or through the insertion of viral regulatory sequences that can interfere with the function of flanking genes (Varmus *et al.,* 1981). Another concern with the use of defective retrovirus vectors is the potential appearance of wild-type replication-competent virus in the packaging cells. This may result from recombination events in which the intact sequence from the recombinant virus inserts upstream from the *gag, pol, env* sequence integrated in the host cell genome. However, new packaging cell lines are now available that should greatly decrease the likelihood of recombination (Markowitz *et al.,* 1988; Hersdorffer *et al.,* 1990).

Other viral vectors may be employed as expression constructs. Vectors derived from viruses such as vaccinia virus (Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.,* 1988), adeno-associated virus (AAV) (Ridgeway, 1988; Baichwal and Sugden, 1986; Hermonat and Muzycska, 1984), and herpes viruses may be employed.

They offer several attractive features for various mammalian cells (Friedmann, 1989; Ridgeway, 1988; Baichwal and Sugden, 1986; Coupar *et al.,* 1988; Horwich *et al.,* 1990).

Several non-viral methods for the transfer of expression constructs into cultured mammalian cells also are contemplated by the present invention. These include calcium phosphate precipitation (Graham and Van Der Eb, 1973; Chen and Okayama, 1987; Rippe *et al.*, 1990), DEAE-dextran (Gopal, 1985), electroporation (Tur-Kaspa *et al.*, 1986; Potter *et al.*, 1984), direct microinjection, DNA-loaded liposomes and lipofectamine-DNA complexes, cell sonication, gene bombardment using high velocity microprojectiles, and receptor-mediated transfection (Wu and Wu, 1987; Wu and Wu, 1988). Some of these techniques may be successfully adapted for *in vivo* or *ex vivo* use.

In a further embodiment of the invention, the expression construct may be entrapped in a liposome. Liposomes are vesicular structures characterized by a phospholipid bilayer membrane and an inner aqueous medium. Multilamellar liposomes have multiple lipid layers separated by aqueous medium. They form spontaneously when phospholipids are suspended in an excess of aqueous solution. The lipid components undergo self-rearrangement before the formation of closed structures and entrap water and dissolved solutes between the lipid bilayers. Also contemplated are lipofectamine-DNA complexes.

Liposome-mediated nucleic acid delivery and expression of foreign DNA *in vitro* has been very successful. Wong *et al.,* (1980) demonstrated the feasibility of liposome-mediated delivery and expression of foreign DNA in cultured chick embryo, HeLa, and hepatoma cells. Nicolau *et al.,* (1987) accomplished successful liposome-mediated gene transfer in rats after intravenous injection.

A number of selection systems may be used including, but not limited to, HSV thymidine kinase, hypoxanthine-guanine phosphoribosyltransferase and adenine phosphoribosyltransferase genes, in *tk-*, *hgprt-* or *aprt-* cells, respectively. Also, anti-metabolite resistance can be used as the basis of selection for *dhfr:* that confers

resistance to methotrexate; *gpt*, that confers resistance to mycophenolic acid; *neo*, that confers resistance to the aminoglycoside G418; and *hygro*, that confers resistance to hygromycin.

Pharmaceutical compositions

Where clinical applications are contemplated, it may be necessary to prepare pharmaceutical compositions - expression vectors, virus stocks, proteins, antibodies and drugs - in a form appropriate for the intended application. Generally, this will entail preparing compositions that are essentially free of impurities that could be harmful to humans or animals.

One generally will desire to employ appropriate salts and buffers to render delivery vectors stable and allow for uptake by target cells. Buffers also are employed when recombinant cells are introduced into a patient. Aqueous compositions of the present invention comprise an effective amount of the protein or peptide, dissolved or dispersed in a pharmaceutically acceptable carrier or aqueous medium. Such compositions also are referred to as innocula. The phrase "pharmaceutically or pharmacologically acceptable" refers to molecular entities and compositions that do not produce adverse, allergic, or other untoward reactions when administered to an animal or a human. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the proteins or peptides of the present invention, its use in therapeutic compositions is contemplated. Supplementary active ingredients also can be incorporated into the compositions.

The active compositions of the present invention may include classic pharmaceutical preparations. Administration of these compositions according to the present invention are via any common route so long as the target tissue is available via that route. This includes oral, nasal, buccal, rectal, vaginal or topical. Alternatively,

administration may be by orthotopic, intradermal, subcutaneous, intramuscular, intraperitoneal, intraarterial or intravenous injection. Such compositions normally would be administered as pharmaceutically acceptable compositions, described *supra*.

The pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersions. In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and vegetable oils. The proper fluidity can be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it is preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions are prepared by incorporating the active compounds in the required amount in the appropriate solvent with various other ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the various sterilized active ingredients into a sterile vehicle which contains the basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum-drying and freeze-drying techniques which yield a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Therapeutic agents

In certain embodiments, chemotherapeutic agents may be attached to a targeting peptide or fusion protein for selective delivery to a tumor. Agents or factors suitable for use may include any chemical compound that induces DNA damage when applied to a cell. Chemotherapeutic agents include, but are not limited to, 5-fluorouracil, bleomycin, busulfan, camptothecin, carboplatin, chlorambucil, cisplatin (CDDP), cyclophosphamide, dactinomycin, daunorubicin, doxorubicin, estrogen receptor binding agents, etoposide (VP16), farnesyl-protein transferase inhibitors, gemcitabine, ifosfamide, mechlorethamine, melphalan, mitomycin, navelbine, nitrosurea, plicomycin, procarbazine, raloxifene, tamoxifen, taxol, temazolomide (an aqueous form of DTIC), transplatinum, vinblastine and methotrexate, vincristine, or any analog or derivative variant of the foregoing. Most chemotherapeutic agents fall into the following categories: alkylating agents, antimetabolites, antitumor antibiotics, corticosteroid hormones, mitotic inhibitors, and nitrosoureas, hormone agents, miscellaneous agents, and any analog or derivative variant thereof.

Chemotherapeutic agents and methods of administration, dosages, etc. are well known to those of skill in the art (see for example, the "Physicians Desk Reference", Goodman & Gilman's "The Pharmacological Basis of Therapeutics" and in "Remington's Pharmaceutical Sciences", incorporated herein by reference in relevant parts), and may be combined with the invention in light of the disclosures herein. Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Examples of specific chemotherapeutic agents and dose regimes are also described herein. Of course, all of these dosages and agents described herein are exemplary rather than limiting, and other doses or agents may be used by a skilled artisan for a specific patient or application. Any dosage in-between these points, or range derivable therein is also expected to be of use in the invention.

Alkylating agents

Alkylating agents are drugs that directly interact with genomic DNA to prevent the cancer cell from proliferating. This category of chemotherapeutic drugs represents agents that affect all phases of the cell cycle, that is, they are not phase-specific. An alkylating agent, may include, but is not limited to, a nitrogen mustard, an ethylenimene, a methylmelamine, an alkyl sulfonate, a nitrosourea or a triazines. They include but are not limited to: busulfan, chlorambucil, cisplatin, cyclophosphamide (cytoxan), dacarbazine, ifosfamide, mechlorethamine (mustargen), and melphalan.

Antimetabolites

Antimetabolites disrupt DNA and RNA synthesis. Unlike alkylating agents, they specifically influence the cell cycle during S phase. Antimetabolites can be differentiated into various categories, such as folic acid analogs, pyrimidine analogs and purine analogs and related inhibitory compounds. Antimetabolites include but are not limited to, 5-fluorouracil (5-FU), cytarabine (Ara-C), fludarabine, gemcitabine, and methotrexate.

Natural Products

Natural products generally refer to compounds originally isolated from a natural source, and identified has having a pharmacological activity. Such compounds, analogs and derivatives thereof may be, isolated from a natural source, chemically synthesized or recombinantly produced by any technique known to those of skill in the art. Natural products include such categories as mitotic inhibitors, antitumor antibiotics, enzymes and biological response modifiers.

Mitotic inhibitors include plant alkaloids and other natural agents that can inhibit either protein synthesis required for cell division or mitosis. They operate during a specific phase during the cell cycle. Mitotic inhibitors include, for example, docetaxel, etoposide (VP16), teniposide, paclitaxel, taxol, vinblastine, vincristine, and vinorelbine.

Taxoids are a class of related compounds isolated from the bark of the ash tree, *Taxus brevifolia*. Taxoids include but are not limited to compounds such as docetaxel and paclitaxel. Paclitaxel binds to tubulin (at a site distinct from that used by the vinca alkaloids) and promotes the assembly of microtubules.

Vinca alkaloids are a type of plant alkaloid identified to have pharmaceutical activity. They include such compounds as vinblastine (VLB) and vincristine.

Antitumor Antibiotics

Antitumor antibiotics have both antimicrobial and cytotoxic activity. These drugs also interfere with DNA by chemically inhibiting enzymes and mitosis or altering cellular membranes. These agents are not phase specific so they work in all phases of the cell cycle. Examples of antitumor antibiotics include, but are not limited to, bleomycin, dactinomycin, daunorubicin, doxorubicin (Adriamycin), plicamycin (mithramycin) and idarubicin.

Hormones

Corticosteroid hormones are considered chemotherapy drugs when they are implemented to kill or slow the growth of cancer cells. Corticosteroid hormones can increase the effectiveness of other chemotherapy agents, and consequently, they are frequently used in combination treatments. Prednisone and dexamethasone are examples of corticosteroid hormones.

Progestins such as hydroxyprogesterone caproate, medroxyprogesterone acetate, and megestrol acetate have been used in cancers of the endometrium and breast. Estrogens such as diethylstilbestrol and ethinyl estradiol have been used in cancers such as breast and prostate. Antiestrogens such as tamoxifen have been used in cancers such as breast. Androgens such as testosterone propionate and fluoxymesterone have also been used in treating breast cancer. Antiandrogens such as flutamide have been used in the treatment of prostate cancer. Gonadotropin-releasing hormone analogs such as leuprolide have been used in treating prostate cancer.

Miscellaneous Agents

Some chemotherapy agents do not fall into the previous categories based on their activities. They include, but are not limited to, platinum coordination complexes, anthracenedione, substituted urea, methyl hydrazine derivative, adrenalcortical suppressant, amsacrine, L-asparaginase, and tretinoin. It is contemplated that they may be used within the compositions and methods of the present invention.

Platinum coordination complexes include such compounds as carboplatin and cisplatin (*cis*-DDP).

An anthracenedione such as mitoxantrone has been used for treating acute granulocytic leukemia and breast cancer. A substituted urea such as hydroxyurea has been used in treating chronic granulocytic leukemia, polycythemia vera, essental thrombocytosis and malignant melanoma. A methyl hydrazine derivative such as procarbazine (N-methylhydrazine, MIH) has been used in the treatment of Hodgkin's disease. An adrenocortical suppressant such as mitotane has been used to treat adrenal cortex cancer, while aminoglutethimide has been used to treat Hodgkin's disease.

Regulators of Programmed Cell Death

Apoptosis, or programmed cell death, is an essential process for normal embryonic development, maintaining homeostasis in adult tissues, and suppressing carcinogenesis (Kerr et al., 1972). The Bcl-2 family of proteins and ICE-like proteases have been demonstrated to be important regulators and effectors of apoptosis in other systems. The Bcl-2 protein, discovered in association with follicular lymphoma, plays a prominent role in controlling apoptosis and enhancing cell survival in response to diverse apoptotic stimuli (Bakhshi et al., 1985; Cleary and Sklar, 1985; Cleary et al., 1986; Tsujimoto et al., 1985; Tsujimoto and Croce, 1986). The evolutionarily conserved Bcl-2 protein now is recognized to be a member of a family of related proteins, which can be categorized as death agonists or death antagonists.

Subsequent to its discovery, it was shown that Bcl-2 acts to suppress cell death triggered by a variety of stimuli. Also, it now is apparent that there is a family of Bcl-2 cell death regulatory proteins which share in common structural and sequence homologies. These different family members have been shown to either possess similar functions to Bcl-2 (e.g., Bcl_{XL}, Bcl_W, Bcl_S, Mcl-1, A1, Bfl-1) or counteract Bcl-2 function and promote cell death (e.g., Bax, Bak, Bik, Bim, Bid, Bad, Harakiri).

Non-limiting examples of pro-apoptosis agents contemplated within the scope of the present invention include gramicidin, magainin, mellitin, defensin, cecropin, $(KLAKLAK)_2$ (SEQ ID NO:1), $(KLAKKLA)_2$ (SEQ ID NO:2), $(KAAKKAA)_2$ (SEQ ID NO:3) or $(KLGKKLG)_3$ (SEQ ID NO:4).

Angiogenic inhibitors

In certain embodiments the present invention may concern administration of targeting peptides attached to anti-angiogenic agents, such as angiotensin, laminin peptides, fibronectin peptides, plasminogen activator inhibitors, tissue metalloproteinase inhibitors, interferons, interleukin 12, platelet factor 4, IP-10, Gro-ß, thrombospondin, 2-methoxyoestradiol, proliferin-related protein, carboxiamidotriazole, CM101, Marimastat, pentosan polysulphate, angiopoietin 2 (Regeneron), interferon-alpha, herbimycin A, PNU145156E, 16K prolactin fragment, Linomide, thalidomide, pentoxifylline, genistein, TNP-470, endostatin, paclitaxel, accutin, angiostatin, cidofovir, vincristine, bleomycin, AGM-1470, platelet factor 4 or minocycline.

Dosages

The skilled artisan is directed to "Remington's Pharmaceutical Sciences" 15th Edition, chapter 33, and in particular to pages 624-652. Some variation in dosage will necessarily occur depending on the condition of the subject being treated. The person responsible for administration will, in any event, determine the appropriate dose for the individual subject. Moreover, for human administration, preparations should meet

sterility, pyrogenicity, and general safety and purity standards as required by the FDA Office of Biologics standards.

EXAMPLES

The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered by the inventors to function well in the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Example 1. Bone Marrow Targeting Peptides

A non-limiting example of an organ of specific interest for targeting petides is bone marrow. Bone is the preferred site of metastasis in the large majority of patients with prostate cancer (Fidler, 1999). This striking selectivity has been viewed as an example of site-specific interactions that were essential to cancer progression (Rak, 1995; Zetter, 1998). Despite the clinical relevance, little is known about the mechanisms that control prostate cancer spread to bone. In addition, there were no effective strategies for targeting therapeutic agents for the treatment of metastatic prostate cancer (Brodt et. al, 1996).

A subset of peptides capable of selective homing to bone marrow through the circulation is likely to simulate the behavior of prostate cancer cells during bone metastasis formation. The vascular markers targeted by using phage display might also be utilized by tumor cells to metastasize. This concept has already been proven to be true for lung-homing peptides. Peptides that home to lung blood vessels inhibit experimental metastasis. These results fit a "modified seed and soil" model, in which the basis for site-specific metastasis is the presence of homing receptors in blood

vessels of certain tissues to which metastasis preferentially occurs. Such selective vascular markers are exposed to tumor cells during adhesion, the first step of the metastastic cascade. Isolation of bone marrow-homing peptides is of utility for identifying those vascular markers that mediate prostate cancer cell homing during the metastatic process, and for potential therapeutic intervention in preventing metastases to bone, or in selectively imaging and/or treating cancer that has already metastasized to bone.

Methods

In vivo screening of phage libraries was used to isolate peptides that bind to bone marrow in mice. The bone marrow targeting peptides were characterized with regard to their ability to inhibit metastasis in prostate cancer mouse models. Affinity chromatography and molecular cloning were used to identify the receptors for the bone-marrow binding peptides. The compositions and methods disclosed herein were of use to develop new anti-prostate cancer therapeutic strategies that focus on the prevention and treatment of bone metastasis.

In vivo screenings to isolate peptides that home to bone marrow in mice.

Phage libraries were injected intravenously. The libraries were prepared according to the protocol of Smith and Scott (1985) with improvements, discussed below. The phage in these libraries displayed inserts ranging from 5 to 11 residues. Tissue samples were processed for phage rescue by transfer to 1ml DMEM-PI in a glass tube and homogenized with a grinder. Bone marrow does not require homogenization, whereas other organs that were used as controls needed to be minced before they could be efficiently homogenized. Samples were transferred to autoclaved 2 ml Eppendorf tubes. The tissues were washed with ice cold DMEM-PI containing 1% BSA. After 3 washes, the pellets were resuspended and brought to 37°C before adding bacteria. Incubation of the washed tissue samples with 1.5 ml of competent K91-kan bacteria (OD_{600} 0.2 in 1:10 dil.) for one hour at room temperature was used for recovering the phage particles.

Multiple aliquots were plated in LB tet/kan plates or dishes containing 40 μg/ml of tetracycline and 100μg/ml kanamycin. Platings were performed at several concentrations, covering a large range of sample, *i.e.* 3 ml, 1 ml, 300μl, 100μl, 30 μl. The beads that were used for plating were passed on to two subsequent 10cm LB tet/kan plates so as to recover every potentially phage infected bacterial clone trapped on the bead surface. The dishes were incubated overnight at 37°C. The remaining 2 –3 ml of infected culture (including the homogenized tissue) was transferred into 10 ml of LB medium containing 40 μg/ml tetracycline and 100 μg/ml kanamycin (LB tet/kan) and placed in the shaker at 37°C for 2h. The 12 ml cultures were expanded to 1 liter LB tet/kan and grown overnight in the 37°C shaker. Phage were rescued from the bulk amplified bacterial culture after 12-16 h, according to standard protocols and saved for subsequent rounds of selection. From the plates/dishes in the incubator, well separated colonies from bone marrow were sequenced. The colonies were transferred to 96 well plates containing 20μl PBS/well for sequencing

Immunohistochemical staining with an anti-M13 antibody was used to examine phage targeting in various tissues (Pasqualini and Ruoslahti, 1996; Arap et al, 1998). The phage were injected IV and allowed to circulate for 5 min or 24 h. Mice in the 5 min experiment were perfused with DMEM after the phage injection to remove unbound phage from the circulation. There was little circulating phage after 24 h (Arap et al, 1998a, 1998b). The animals were sacrificed, their tissues collected, fixed with Bouin's solution, sectioned and stained with antibodies against the phage.

Results

Murine bone marrow targeting in vivo in mice

Bone marrow targeting sequence motifs were identified by intravenously injecting phage libraries into mice and recovering phage from bone marrow. Phage were injected intravenously, recovered from the bone marrow, repeatedly amplified in vitro and re-injected to obtain sufficient enrichment. After three rounds of selection, phage preparations that homed to mouse bone marrow were obtained. The individual phage exhibited similar organ specificity as the pooled phage after intravenous

injection. Several peptide motifs were identified and characterized. The most promising motifs that show specificity in vivo are shown in Table 3

Table 3. Sequences in phage that target murine bone marrow in vivo.

$CX_3CX_3CX_3C$ peptide library

C V M T **C A P R C** F E H C (SEQ ID NO:5)

C D G V **C A P R C** G E R C (SEQ ID NO:6)

C T G G C V V D C L S I C (SEQ ID NO:7)

C G V P **C R P A C** R G L C (SEQ ID NO:8)

C A G F C V P G C H S K C (SEQ ID NO:9)

C A G A C P V G C G T G C (SEQ ID NO:10)

X6 peptide library

A E **R L W R** S (SEQ ID NO:11)

S Q H V V S G (SEQ ID NO:12)

I A **W R L** E H (SEQ ID NO:13)

W Y T V M S W (SEQ ID NO:14)

R L T Y K L Q (SEQ ID NO:15)

W Q **R L** Y A W (SEQ ID NO:16)

E F **R L** G S K (SEQ ID NO:17)

L G S N S K A (SEQ ID NO:18)

C G V V K F A (SEQ ID NO:19)

The skilled artisan will realize that the bone marrow targeting peptide sequences identified herein will be of use for numerous applications within the scope of the present invention, including but not limited to targeted delivery of therapeutic agents or gene therapy, *in vivo* imaging of normal or diseased organs, tissues or cell types,

identification of receptors and receptor ligands in organs, tissues or cell types, and therapeutic treatment of a number of human diseases, particularly metastatic prostate cancer.

Example 2. Prostate and Prostate Cancer targeting peptides

Another non-limiting organ of particular interest for targeting is the prostate. Prostate is an unusual organ because it continues to growth throughout adult life. As a result, benign prostate hypertrophy (BPH) affects most elderly men to some degree. Even more serious, the prostate is a frequent site of malignant tumors. One out of eleven men will develop prostate cancer during their lifetime. Because serum markers for prostate cancer were available, many of these malignant tumors were currently detected early in the course of the disease. In the absence of reliable ways of predicting which ones will progress clinically, many were aggressively treated with surgery or radiotherapy, often with devastating side-effects such as incontinence and impotence (Lane and Shah, 1999; Mikolajczyk et al., 2000). There is a clear need for improved methods for detection, prognosis, and treatment of human prostate cancer.

Many interesting genes in the prostate may be expressed in restricted--but perhaps highly specific or accessible--cellular locations such as the prostate vasculature. Thus, potential targets for intervention may easily be overlooked by high-throughput sequencing or gene array approaches that do not account for the molecular heterogeneity intrinsic to microanatomic or physiological contexts.

The methods of the present invention allow the identification of peptides that home to specific target sites *in vivo* (Pasqualini et al., 1996, 1997, Koivunen et al., 1999; Pasqualini, 1999). *In vivo* selection of phage peptide libraries yields peptides that are capable of homing to specific receptors in target tissues through the circulation. These studies have revealed a surprising degree of specialization in various normal tissues (Pasqualini, 1999; Rajotte et al., 1998, 1999). The present example concerns compositions and methods of use of prostate targeting peptides.

Methods

In vivo phage targeting of the prostate

Phage display libraries were injected intravenously. Samples were kept on ice at all times. Prostate tissue samples were processed as follows. The first sample was stored at –80°C as a backup. The second sample was processed for histology/pathology and HE or anti-M13 phage immunostaining. The third sample was divided under clean conditions to obtain three fragments with the same weight.

The triplicates from the third prostate sample were processed for host bacterial infection and phage recovery. The prostate sample was transferred to 1 ml DMEM-protease inhibitors (PI) in a glass tissue grinder, homogenized and transfered cell suspension to an autoclaved 2 ml eppendorf tube. Next, the prostate tissue samples were washed three times with ice cold DMEM-PI containing 1% BSA. The tissue was mixed with DMEM-PI and vortexed for 30 seconds after each wash. After spinnig at 4,000 rpm for 3 min and the supernatant was carefully discarded (the tissue pellet should remain undisturbed). Next, 1.5 ml DMEM-PI/BSA was added. After the third wash, the pellet was briefly vortexed to re-suspend the dissolved pellet warmed briefly to 37° before adding the host bacteria. Then, the admixture was incubated with 1.5 ml of competent K91-kan bacteria (OD_{600} = 2) for one hour at room temperature.

The admixture was transferred to Falcon tubes containing 10 ml of LB medium plus 0.2 μg/ml of tetracycline at RT for 20 minute. Multiple aliquots were plated in LB tet/kan plates or dishes containing 40 μg/ml of tetracycline and 100 μg/ml kanamycin. Finally, dishes were incubated at 37°C and the phage transducing unit count determined after an overnight incubation.

Prostate Cancer Targeting

Tumor blood vessels are known to be leaky. Longer term exposure of the mouse subject to a phage display library may result in migration of phage and binding to prostate cancer cell markers. Mice were incubated with a phage library for 24 hrs to target cancer cell markers.

Male nude mice (4 mice) were injected with 10^6 DU-145 cells in PBS. After tumor growth, the mice were injected with either a CX10C phage display library. After allowing the library to circulate for 24 hours, the mice were sacrificed and tissue samples were collected. Samples were homogenized in Dounce homogenizer and K91 bacteria were added to recover phage. Bacteria were plated on kan/tet LB plates in triplicate at a series of dilution. The remaing tumor homogenate with bacteria was incubated for 1 hr at RT with 10 ml of LB/tet/kan. Another 10 ml of LK/tet/kan and incubated at 37°C in a rotator to provide bulk phage stock.. 216 colonies were picked from the plates to make a combined stock for second round screening. After the clones wer amplified, they were pooled and phage were precipitated with PEG/NaCl. Nude mice bearing prostate tumors were subjected to a second round of selection as described above, using the pooled phage recovered from round 1. A third round of screening was perfromed as described.

Results

Normal Mouse Prostate

Mouse prostate targeting peptide motifs obtained by the methods disclosed above are shown in Table 4.

Table 4. Mouse Prostate Targeting Peptides Obtained by *In vivo* Phage Display

RVGTWGR	SEQ ID NO:20	YICPGPC	SEQ ID NO:30
GRGRWGS	SEQ ID NO:21	SYQSPGP	SEQ ID NO:31
VQGIGRL	SEQ ID NO:22	AAAGSKH	SEQ ID NO:32
VGSGRLS	SEQ ID NO:23	GSRIRTP	SEQ ID NO:33
GWTVRDG	SEQ ID NO:24	SWGSRIR	SEQ ID NO:34
GSRIRTP	SEQ ID NO:25	GGGSRIS	SEQ ID NO:35
GGGSRIS	SEQ ID NO:26	RVVGSRS	SEQ ID NO:36
VMGGVVS	SEQ ID NO:27	DGSTNLS	SEQ ID NO:37

YGNDRRN SEQ ID NO:28 VGSGRLS SEQ ID NO:38

SGKDRRS SEQ ID NO:29

Prostate Cancer

By the third round of *in vivo* screening, phage were obtained that exhibited high selectivity for tumor localization compared to control normla kidney tissue (not shown). Prostate cancer targeting sequences identified by DNA sequencing the phage inserts are listed in Table 5.

Table 5. Prostate cancer targeting peptides

LSRLVTGDVIC (SEQ ID NO:210)

CGNMGGSLYYVC (SEQ ID NO:211)

CLHWEATFNPQC (SEQ ID NO:212)

CRTEVWRSNQRC (SEQ ID NO:213)

CHVRDEHHEQGC (SEQ ID NO:214)

CPMQATRNLWHC (SEQ ID NO:215)

CRDDAKVMRYNC (SEQ ID NO:216)

CNNWGELLGFNC (SEQ ID NO:217)

CEGGYENLVLKC (SEQ ID NO:218)

CRNAWNKHGSRC (SEQ ID NO:219)

CKERMYREQRRC (SEQ ID NO:220)

CRTIDIENNELC (SEQ ID NO:221)

CHRGINRSTTDC (SEQ ID NO:222)

CETGREIDRSDC (SEQ ID NO:223)

CCGRKTRGVAIC (SEQ ID NO:224)

CLASMLNMSTLC (SEQ ID NO:225)

CGQGFAPRNLVC (SEQ ID NO:226)

CLGKWKSSRGTC (SEQ ID NO:227)

CGEGFGSEWPPC (SEQ ID NO:228)

CKPDYMDSNKMC (SEQ ID NO:229)

CTRNITKSRMMC (SEQ ID NO:230)

CVRNVDQNTNTC (SEQ ID NO:231)

CFWTRENRGWTC (SEQ ID NO:232)

CRIRGIQLRPAC (SEQ ID NO:233)

CEVGLSAAMAYCC (SEQ ID NO:234)

The skilled artisan will realize that the prostate targeting peptide sequences identified herein will be of use for numerous applications within the scope of the present invention, including but not limited to targeted delivery of therapeutic agents or gene therapy, *in vivo* imaging of normal or diseased organs, tissues or cell types, identification of receptors and receptor ligands in organs, tissues or cell types, and therapeutic treatment of a number of diseases, particularly prostate cancer.

Example 3. Identification of mouse placenta, adipose, ovary and ureter targeting peptides

Identification of placenta homing peptides

Peptides homing to the mouse placenta were identified by a post-clearing protocol using a phage display library. A first round of biopanning was performed on pregnant mice. Samples of placenta were removed and phage rescued according to the standard protocols described above, with one modification. In the typical bipanning protocol, thousands of phage may be recovered from a single organ, tissue or cell type. Typically, between 200 and 300 individual colonies were selected from plated phage and these were amplified and pooled to form the phage display library for the second or third rounds of biopanning. In this example, all phage rescued from the first round of biopanning were amplified in bulk on solid medium and then pooled to form the phage

display library for the second round of biopanning. That is, there was no restriction of the rescued phage from the first round of biopanning. This *in vivo* biopanning without restriction was performed for three rounds (rounds I-III), then a post-clearing procedure was used.

In the post-clearing protocol (round IV), phage were administered to a non-pregnant mouse. Phage that bound to tissues other than placenta were absorbed from the circulation. Remaining phage were recovered from the plasma of the non-pregnant mouse. This protocol was designed to isolate phage that bound to placenta but not to other mouse organs, tissues or cell types. The following placenta targeting peptides were identified, along with their frequencies. A search of the GenBank database disclosed that none of the SEQ ID NO's listed below was 100% homologous with any known peptide sequence.

TPKTSVT (SEQ ID NO:39) 7.4% in round III, 8.5% in round IV

RMDGPVR (SEQ ID NO:40) 3.1% in round III, 8.5% in round IV

RAPGGVR (SEQ ID NO:41) <1% in round III, 8.5% in round IV

VGLHARA (SEQ ID NO:42) 4.2% in round III, 7.4% in round IV

YIRPFTL (SEQ ID NO:43) 2.1% in round III, 5.3% in round IV

LGLRSVG (SEQ ID NO:44) <1% in round III, 5.3% in round IV

PSERSPS (SEQ ID NO:45) (data not available)

As can be seen, the use of a post-clearing procedure resulted in a substantial enrichment of phage bearing placenta targeting peptides. Although this procedure was used for placenta, the skilled artisan will realize that post-clearance can be performed on for any organ, tissue or cell type where a phage library can be administered to a subject lacking that organ, tissue or cell type. For example, a post-clearing procedure for prostate or testicle targeting peptides could be performed in a female subject, and for ovary, vagina or uterus in a male subject.

A homology search identified several candidate proteins as endogenous analogs of the placental targeting peptides, including TCR gamma-1 (TPKTSVT, SEQ ID NO:39), tenascin (RMDGPVR, SEQ ID NO:40 and RAPGGVR, SEQ ID NO:41), MHC Class II (LGLRSVG, SEQ ID NO:44), angiotensin I (YIRPFTL, SEQ ID NO:43) and MHC H2-D-q alpha chain (VGLHARA, SEQ ID NO:42).

Validation of placenta homing peptides and inhibition of pregnancy

The placenta homing peptides were validated *in vivo* by injection into pregnant mice and recovery from the placenta. FIG. 1 shows the results of the validation studies for selected placenta homing phage. The phage clones are identified as: PA - TPKTSVT (SEQ ID NO:39), PC - RAPGGVR (SEQ ID NO:41), PE - LGLRSVG (SEQ ID NO:44), PF - YIRPFTL (SEQ ID NO:43). It can be seen that the PA clone exhibited placental homing more than an order of magnitude greater than observed with control fd-tet phage. The PC clone also showed substantially higher placental localization, while the PE and PF clones were not substantially enriched in placenta compared to control phage.

Despite the absence of apparent enrichment of the PF clone in placental tissue, both the PA and PF peptides showed anti-placental activity. Table 6 shows the effects of the PA and PF placental targeting peptides injected into pregnant mice, attached to FITC (fluorescein isothiocyanate), GST (glutathion S-transferase) or to phage. At lower dosages (450 μg total), FITC conjugated PA and PF showed a slight effect on pregnancy (Table 6). At higher dosages (800 to 1000 μg protein or 4.5×10^{10} phage), both protein and phage conjugated PA and PF peptides substantially interfered with fetal development (Table 6), apparently resulting in death of the fetuses in most cases. The CARAC peptide (SEQ ID NO:46), an adipose targeting peptide (FE, TREVHRS, SEQ ID NO:47) or fd-tet phage were used as non-placental targeting controls.

Table 6. Effect of placental targeting peptides on fetal development

Inhibition with FITC conjugates –I

1 mouse injected iv (predominantly) or ip ~every other day, day 1-day 18, 9 times, Total 450mM (~450μg)

Peptide Injected	Pregnancy Outcome	Peptide Effect on Embryo
CARAC-FITC (- control)	Delivery: 18d, 5 normal pups	No effect
PA-FITC (placenta homer)	Delivery: 19d, 8 normal pups	No effect
PF-FITC (placenta homer)	Delivery: 21d, 1 dead pup	Development delay, toxicity

Inhibition with FITC conjugates –II

1 mouse injected sc (predominantly) or iv ~every other day, day 4-day 17, 10 times, Total 1M (~1mg)

Peptide Injected	Pregnancy Outcome	Peptide Effect on Embryo
CARAC-FITC (- control)	Delivery: 20d, 5 pups, 1-dead	Slight toxicity?
PA-FITC (placenta homer)	No fetuses inside after 21 d	Pregnancy termination
PF-FITC (placenta homer)	No fetuses inside after 21 d	Pregnancy termination

Inhibition with phage conjugates –I

1 mouse injected iv (predominantly) or ip ~every other day, day 1-day 18, 9 times, Total $4.5x10^{10}$ TU

Peptide Injected	Pregnancy Outcome	Peptide Effect on Embryo
Fd-Tet (- control)	Avertin OD=>death. fetuses-OK	?
PA-phage (placenta homer)	Delivery: 24d, 4 pups, 1-dead	Development delay, toxicit
PF-phage (placenta homer)	Delivery: 25d, 8 pups, all dead	Development delay, toxicit

Inhibition with GST conjugates –I

1 mouse injected sc (predominantly) or iv ~every other day, day 4-day 17, 10 times, Total 800μg

Peptide Injected	Pregnancy Outcome	Peptide Effect on Embry
GST-FE (- control)	Delivery: 20d, 2 pups,OK	No effect
GST-PA (placenta homer)	No delivery or fetuses after 21 d	Pregnancy termination
GST-PF (placenta homer)	Day 15: no fetuses inside, uterus necrotic	Pregnancy termination

These results validate the placental targeting peptide sequences identified above. They further demonstrate that even in the absence of substantial enrichment of phage bearing the targeting sequence to the target organ (*e.g.* peptide PF, FIG. 1), the targeting peptide may nevertheless provide for targeted delivery of therapeutic agents to the target organ. In this study, it appeared that at lower dosages the PF peptide was more effective than the PA peptide at interfering with pregnancy, despite the observation that the PA peptide produced a many-fold higher level of phage localization to placenta.

The skilled artisan will realize that the disclosed methods and peptides may be of use for targeted delivery of therapeutic agents to the fetus through the placenta, as well as for novel approaches to terminating pregnancy.

Adipose targeting peptides

A similar procotol was used to isolate fat targeting peptides from a genetically obese mouse (Zhang et al., 1994; Pelleymounter et al., 1995), with post-clearing performed in a normal mouse. The fat-targeting peptides isolated included TRNTGNI (SEQ ID NO:48), FDGQDRS (SEQ ID NO:49); WGPKRL (SEQ ID NO:50); WGESRL (SEQ ID NO:51); VMGSVTG (SEQ ID NO:52), KGGRAKD (SEQ ID

NO:53), RGEVLWS (SEQ ID NO:54), TREVHRS (SEQ ID NO:47) and HGQGVRP (SEQ ID NO:55).

Homology searches identified several candidate proteins as the endogenous analogs of the fat targeting peptides, incliuding stem cell growth factor (SCGF) (KGGRAKD, SEQ ID NO:53), attractin (mahogany) (RGEVLWS, SEQ ID NO:54), angiopoitin-related adipose factor (FIAF) (TREVHRS, SEQ ID NO:47), adipophilin (ADRP) (VMGSVTG, SEQ ID NO:52), Flt-1 or procollagen type XVII (TRNTGNI, SEQ ID NO:48) and fibrillin 2 or transferrin-like protein p97 (HGQGVRP, SEQ ID NO:55)

Validation of adipose targeting peptides

The fat homing peptides were validated by *in vivo* homing, as shown in FIG. 2. The fat homing clones selected were: FA - KGGRAKD (SEQ ID NO:53), FC – RGEVLWS (SEQ ID NO:54), FE – TREVHRS (SEQ ID NO:47) and FX – VMGSVTG (SEQ ID NO:52). As seen in FIG. 2, all of these clones exhibited some elevation of homing to adipose tissue, with clone FX showing several orders of magnitude higher adipose localization than control fd-tet phage. Clone FX also exhibited substantially higher localization than the other selected fat homing clones. However, by analogy with the placental homing peptides disclosed above, the skilled artisan will realize that fat homing clones exhibiting lower levels of adipose tissue localization may still be of use for targeted delivery of therapeutic agents.

The skilled artisan will realize that targeting peptides selective for angiogenic vasculature in adipose tissue could be of use for weight reduction or for preventing weight gain. By attaching anti-angiogenic or toxic moieties to an adipose targeting peptide, the blood vessels supplying new fat tissue could be selectively inhibited, preventing the growth of new deposits of fat and potentially killing existing fat deposits.

Ovary and ascites targeting peptides

Additional targeting peptide sequences have been identified against mouse ovary and ascites fluid, listed below.

Mouse ovary targeting peptides include GLAKLIP (SEQ ID NO:56), HLISDMS (SEQ ID NO:57), LQHWLLS (SEQ ID NO:58), ALVLQG (SEQ ID NO:59). TGVALQS (SEQ ID NO:60), YVQSREG (SEQ ID NO:61), PLFWPYS (SEQ ID NO:62), DGSG (SEQ ID NO:63), EGSG (SEQ ID NO:64), SSPRPGV (SEQ ID NO:65), DGYPAIA (SEQ ID NO:66) GHAIE (SEQ ID NO:67) and IWSTSER (SEQ ID NO:68).

Targeting peptides against mouse ascites include YRLRG (SEQ ID NO:69), YRARG (SEQ ID NO:70), SQPLG (SEQ ID NO:71), SQPWG (SEQ ID NO:72), QRLVTP (SEQ ID NO:73), QVLVTP (SEQ ID NO:74), QRLVHP (SEQ ID NO:75), QVLVHP (SEQ ID NO:76), ITRWRYL (SEQ ID NO:77), SLGGMSG (SEQ ID NO:78), SQLAAG (SEQ ID NO:79), SLLAAG (SEQ ID NO:80), SQLVAG (SEQ ID NO:81), SLLAAG (SEQ ID NO:82), GLPSGLL (SEQ ID NO:83), HGGSANP (SEQ ID NO:84), SLEAFFL (SEQ ID NO:85), CVPELGHEC (SEQ ID NO:86), CELGFELGC (SEQ ID NO:87) AND CFFLRDWFC (SEQ ID NO:88).

Ureter targeting peptides

Similar protocols were used to identify ureter targeting peptides in C57Bl mice, disclosed in Table 7.

Table 7. Ureter targeting peptides

Motif	**Peptide**
LRXGN	GVMLRRG (SEQ ID NO:238)
(SEQ ID NO:235)	YSLRIGL (SEQ ID NO:239)
	LRDGNGE (SEQ ID NO:240)
	CLRGGNLR (SEQ ID NO:241)
RGAG	VRGLAAA (SEQ ID NO:242)
(SEQ ID NO:236)	ARGAGLA (SEQ ID NO:243)

	RGAGTGWT (SEQ ID NO:244)
	ARGVNGA (SEQ ID NO:245)
DLLR	DLLRARW (SEQ ID NO:246)
(SEQ ID NO:237)	DLLRTEW (SEQ ID NO:247)
	EFDLVRQ (SEQ ID NO:248)
none	GCDEGGG (SEQ ID NO:249)
none	GDSPVES (SEQ ID NO:250)

Example 4: Screening an alpha-spleen antibody library *in vivo* by BRASIL

Targeting peptides against spleen have not been previously identified. As part of the reticulo-endothelial system, biopanning against spleen tissue is complicated by the high background of non-specific phage localization to spleen. The decreased background observed in biopanning with the BRASIL method is advantageous for identifying targeting peptides against tissues such as spleen.

This example demonstrates an illustrative embodiment of the BRASIL method. A phage library based on immunoglobulins derived against the target organ (mouse spleen) was developed and then subjected to *in vivo* biopanning. To construct the immunoglobulin library, mouse spleen was injected into a chicken. After boosting, the chicken spleen was collected and immunoglobulin variable domain sequences were obtained by PCR™ amplification of chicken spleen mRNA. The amplified immunoglobulin variable sequences were inserted into a phage display library (α-library) that was then used for *in vivo* biopanning against mouse spleen. Thus, the spleen targeting peptide sequences obtained from phage localized to mouse spleen *in vivo* were derived from antibody fragments produced in the chicken in response to mouse spleen antigens. The success of this example further shows the broad utility of the BRASIL method. The skilled artisan will realize that the present invention is not limited to the embodiments disclosed herein and that many further developments of the BRASIL methodology are included in the scope of the present invention.

Materials and Methods

Library construction

A white leghorn chicken was immunized with spleen homogenate (about 150 mg per injection) from a perfused (10 ml MEM) Balb/c mouse. The chicken received spleen homogenate boosters at 4 weeks and 8 weeks after the initial immunization. Immune response to mouse spleen by FACS analysis showed that the chicken immune serum contained antibodies against a mouse cell-line (TRAMP-C1). The chicken was sacrificed and its spleen was removed to TRI Reagent (Molecular Research Center, Inc., Cincinatti, OH) 12 weeks after the first immunization.

Total RNA was prepared from the chicken spleen using the manufacturer's protocol for the TRI reagent. cDNA was prepared from the total RNA using oligo(dT)-primers and Superscript enzyme (Life Technologies). cDNAs encoding chicken spleen immunoglobulin variable regions were amplified by CHybVH and ChybIgB (V_{heavy}) or by CSCVK and CHHybL-B (V_{kappa}) primers according to standard techniques. Light chain variable regions and constant regions were PCR™ amplified together using CSC-F and lead-B primers and V_{kappa} and C_{kappa} templates. Heavy chain variable regions and constant regions were PCR™ amplified together using dp-seq and lead-F primers and V_{heavy} and C_{heavy} templates. Heavy- and light -chain fragments were PCR™ amplified together with CSC-F and dp-Ex primers. PCR primers were purchased from Genosys or GenBase, using primer sequences listed in the Cold Spring Harbor laboratory course manual, "Phage Display of Combinatorial Antibody Libraries" (Barbas *et al.*, 2000), the text of which is incorporated herein by reference.

After digestion with Sfi I, the amplification products were ligated to SfiI -digested pComb3x for insertion into the phage library. Ligated pComb3-123 plasmid was electroporated into ER2537 -*E.coli* and phage production was started with subsequent VCM13 (helper phage) infection. The resulting library size was about 5 x 10^6 cfu.

In vivo screening of α-spleen library using BRASIL

Four rounds of *in vivo* screening in mice were performed using the chicken α-spleen library. About 0.8 to 2.0 x 10^{10} TU were injected into a Balb/c mouse. The library was allowed to circulate for 5 minutes. After sacrifice, the mouse spleen was recovered and a single cell suspension was prepared by pressing the spleen through a 70 μm cell strainer nylon mesh. The single cell suspension was centrifuged over oil (9:1 dibutyl phtalate:cyclohexane) using the BRASIL technique and 200 μl of log phase ER2537 *E. coli* were infected with the pellet. Amplified phage recovered from the mouse spleen was used for the subsequent round of screening. No obvious enrichment in the screening rounds was seen in the number of phage homing to spleen and brain compared with the conventional biopanning method, using a piece of spleen obtained prior to BRASIL.

Phage locallized in mouse spleen from the fourth round of screening of the chicken Fab inserts were PCR™ amplified and the PCR product was digested with *Bst* I. Half of the clones out of 90 analyzed produced a similar restriction pattern. Of those, 20 clones were sequenced from which only two had an identical restriction pattern. Four of the antibody based phage clones (numbers 2, 6, 10 and 12) were subjected to further analysis using binding and localization assays.

Testing the clones in vitro using BRASIL:

A singe cell suspension was prepared from two mouse spleens. The suspension was divided into five tubes and incubated on ice with 3x10^9 TU of Fab clones #2, #6, #10, #12 and 2x10^9 TU tet-phage. Phage bound to mouse spleen cells were recovered by BRASIL. 200 μl of log phase ER2537 *E.coli* was infected with the pellet and serial dilutions were plated on LB/carbenicillin and LB/tetracyclin plates for assessment of phage binding. Fd-tet was used as an internal control to normalize all the phage homing experiments.

Testing clones in vivo with BRASIL

Phage ($3x10^9$) of Fab clones #2, #6, #10, #12 and $2x10^9$ TU tet -phage were injected into the tail veins of Balb/c mice and allowed to circulate for 5 minutes. The spleens were recovered and single cell suspensions were prepared on ice from whole spleens. Cell bound phage were recovered by BRASIL. 200 µl of log phase ER2537 *E.coli* was infected with the pellet and serial dilutions were plated on LB/carbenicillin and LB/tetracycline plates for assessment of the phage recovery.

Testing clone #10 versus, control phage NPC-3TT in vivo with BRASIL

Phage ($3x10^9$ TU) of Fab clone #10 and NPC-3TT (control Fab phage) and $1x10^9$ TU of control Fd-tet -phage were injected to mice (2 mice for NPC-3TT, 2 mice for clone #10) and allowed to circulate for 5 minutes. Spleens were recovered and single cell suspensions were prepared on ice. Cell-bound phage were recovered by BRASIL. 200 µl of log phase ER2537 *E.coli* was infected with the pellet and serial dilutions were plated on LB/carbenicillin and LB/tetracycline plates. The NPC-3TT phage is a human anti-tetanus toxin Fab fragment displaying phage.

Homing of Fab clone #10 to spleen versus bone marrow

Phage ($3x10^9$ TU) of Fab clone #10 and NPC-3tt control and $1x10^9$ TU of Fd-tet control phage were injected into mice (2 mice for NPC-3TT, 2 mice for clone #10) and allowed to circulate for 5 minutes. The spleens were recovered and single cell suspensions were prepared. Bone marrow was recovered from the same mice (both femurs) as a control for organ specific homing. Cell-bound phage were recovered by BRASIL.

Fab -fragment production

The plasmid pComb3 containing the chicken Fab inserts was electroporated into ER2537 bacteria. Serial dilutions were plated onto LB/carbenicillin plates and incubated overnight at 37°C. Fab production culture (in super broth with 100 µg/ml carbenicillin) was started from a single plated colony. Fab production was induced with 1 mM IPTG for 7 hours at 30°C. The Fab fragment was purified from the

periplasmic fraction SN2 by affinity purification after determination of the Fab concentration in bacteria supernatant, periplasmic fractions SN1 and SN2 and in the bacteria lysate by ELISA. An α-Fab-Protein G -column was coupled (2mg/ml) with dimethylpimelimidate (DMP) using standard protocols (Harlow and Lane, 1988).

For purifying Fab fragments the following method was used. The SN2 fraction was loaded into a 1 ml HiTrap-protein G-α-Fab-column (Amersham Pharmacia Biotech, Piscataway, NJ) either over 2 hours (if using lower than 50 ml volume with superloop) or overnight (with more than 50 ml volume using a peristaltic pump). The column was washed with 10-20 ml of PBS (phosphate buffered saline). The Fab fragments were eluted with 10 ml of 20 mM glycine buffer, pH 2.2, 150 mM NaCl and 1 ml fractions were collected. Fractions are neutralized with 1 M Tris immediately after elution. Protein concentrations were quantified by A_{280}.

Intravascular staining

To determine *in vivo* distribution of the recovered Fab fragments, 50 to 60 μg of Fab fragment (Fab#10, NPC3-tt or R#16) was injected into the tail vein of a Balb/c mouse and allowed to circulate for 8 minutes. 50 μg of *L.esculentum* lectin-FITC was injected into the mouse and the mouse tissues were fixed by perfusion with 25 to 30 ml of 4% paraformaldehyde/PBS after 2 minutes of lectin circulation. Tissues were removed and post-fixed in 4% paraformaldehyde for 1 hour. Fixed tissues were incubated in 30% sucrose/PBS overnight at 4°C, changing the solution at least twice. The tissues were embedded in the freezing media and frozen on dry ice.

Fixed tissue sections were stained for Fab as follows. Frozen tissue sections (55 μm) were cut on a microtome and washed 3x with PBS. The thin sections were blocked with PBS/0.3%TritonX-100/5% goat serum for 1 hr at room temperature. Sections were incubated overnight at room temperature with 1:400 Cy3 conjugated α-human anti-Fab antibody. The conjugated sections were washed 6x with PBS/0.3% Triton X-100, 3x with PBS, and fixed with 4% paraformaldehyde for 15 minutes. After fixation the sections were washed again 2x with PBS and 2x with distilled water, then mounted on slides using VectorShield.

Results

The *in vitro* localization to mouse spleen cells of phage clones expressing chicken Fab fragments was examined by BRASIL. As shown in FIG. 3, the Fab phage clones isolated by BRASIL showed differential binding to mouse spleen cells compared to Fd-tet insertless control phage. Clone #6 showed the lowest degree of differential binding, similar to the control phage NPC-3TT, which contained a Fab fragment but was not isolated from mouse spleen. Clones #2, #10 and #12 all showed selective binding to mouse spleen cells compared to the Fd-tet control, with at least a two-fold increased binding observed for clones #2 and #10. The amino acid sequences determined for the clone inserts were:

Clone #2:

CQPAMAAVTLDESGGGLQTPGGALSLVCKASGFTFNSYPMGWVRQAPGKGLE WVAVISSSGTTWYAPAVKGRATISRDNGQSTVRLQLSNLRAED (SEQ ID NO:89)

Clone #6:

CQPAMAAVTLDESGGGLQTPGGTLSLVCKASGISIGYGMNWVRQAPGKGLEY VASISGDGNFAHYGAPVKGRATISRDDGQNTVTLQLNNLR (SEQ ID NO:90)

Clone #10:

CQPAMAAVTLDESGGGLQTPGGTLSLVCKGSGFIFSRYDMAWVRQAPGKGLE WVAGIDDGGGYTTLYAPAVKGRATITSRDNGQSTVRLQLNNLR (SEQ ID NO:91)

Clone #12:

ANQPWPPLTLDESGGGLQTPGGALSLVCKASGFTMSSYDMFWVRQAPGKGLE FVAGISSSGSSTEYGAAVKGRATISRDNGQSTVRLQLNNLRAED (SEQ ID NO:92)

A direct comparison was made of *in vitro* phage binding for the Fab clones compared to NPC-3TT. As shown in FIG. 4, clones #2 and #10 exhibited the highest levels of binding to mouse spleen cells *in vitro*. Clones #6 and #12 showed levels of binding to mouse spleen that was only slightly higher than the binding of phage NPC-3TT.

The preferential binding of the chicken Fab phage clones was confirmed by *in vivo* studies using BRASIL. As shown in FIG. 5, selective localization to mouse spleen was even more dramatic *in vivo*, with Fab clones #2, #6 and #10 showing many-fold increased binding to spleen compared to Fd-tet phage. In contrast, Fab clone #12 did not exhibit significantly elevated binding to mouse spleen compared to Fd-tet phage. These results show that *in vitro* results obtained with spleen targeting phage are confirmed *in vivo*.

Fab clone #10 was selected for additional characterization by *in vivo* localization to mouse spleen. The results, shown in FIG. 6, confirm that Fab clone #10 exhibted 3 to 10 fold enrichment in spleen compared to Fd-tet. This effect was not due to general Fab binding, since the Fab control phage NPC-3TT did not exhibit selective localization in spleen compared to Fd-tet insertless phage.

Binding of Fab clone #10 was organ specific, as demonstrated in FIG. 7. Phage from Fab clone #10 and NPC-3TT control were recovered from spleen and bone marrow tissue from the same injected mice. It can be seen in FIG. 7 that Fab clone #10 exhibited selective localization to spleen but not to bone marrow tissue. The control phage did not exhibit selective localization to bone marrow (FIG. 7) or spleen (not shown).

These results show that Fab phage clone #10 selectively targets mouse spleen tissue for binding both *in vitro* and *in vivo*. These results were further validated by vascular staining for *in vivo* phage distribution. Control phage used for this study were clones NPC-3TT (Fab fragment) and clone R#16 (isolated from angiogenic retina screening).

Fab clone #10 was observed to bind to mouse spleen tissue *in vivo* by fluorescent staining (not shown). The control phage NPC-3TT and R#16 did not stain spleen tissue under identical conditions. The clone #10 and NPC-3TT phage were observed to intensively stain kidneys of injected animals, perhaps due to glomerular filtration (not shown). Other control organs (lung, brain, liver, heart and skeletal muscle) did not show staining with clone #10 (not shown).

These results demonstrate that spleen targeting phage peptides can be identified by the BRASIL method. They further show the feasibility of the phage display technique using antibody fragments against a target organ, tissue or cell type to obtain a starting phage library. The ability to obtain targeting peptides against spleen, a tissue that has proven refractory to biopanning using standard phage display protocols because of the high non-specific background, shows the advantages of the BRASIL method.

Example 5: *In vivo* screening of α-Kaposi's sarcoma library in angiogenic retinas

An angiogenic retinal system has been developed as a model for angiogenic tumor tissues. Hypoxia in neonatal mice causes an angiogenic response in the retina. The angiogenic retinal tissue receptors show similarities with angiogenic tumor tissues in phage display binding.

Materials and Methods

Angiogenic model system

One-week-old C57BL/6J mice were exposed to a 75% oxygen atmosphere for 5 days and then kept in room air for another five days. The proliferative neovascular response was quantified by counting the nuclei of new vessels extending from the retina into the vitreous region in 6 μm cross-sections. This model was used to assess binding to newly formed angiogenic vessels of a phage display library injected intravenously

into mice. The peak of neovascularization was observed between postnatal days 17 to 21.

Phage display

A Fab phage library (α-KS) was produced against Karposi's sarcoma tumor tissue that had been immunized into a rabbit, using the same methods disclosed above for spleen. Three rounds of *in vivo* screening were performed using the α-KS library in the angiogenic retinal model system. About 3 to 10 x 10^{10} TU of α-KS phage were injected into 2 C57BL/6 mice with hypoxia-induced retinal neaovascularization on postnatal days 18 to 20. The library was allowed to circulate for 5 minutes. Eyes were enucleated and retinas separated from the rest of the eye. A single cell suspension was prepared from the retinas by crushing them between two glass slides. Single cell suspensions were processed by BRASIL as described above and 200 μl of log phase ER2537 *E.coli* was infected with the pellet. Phage that had been amplified overnight were recovered from the retinal tissue and used for subsequent rounds of screening. The recovery after each round of selection was between 3400-5000 TU.

After three rounds of selection, 90 selected clones were tested for their ability to bind to HUVEC cells. Microtiter wells were coated with HUVECs in complete media. Cells were fixed and incubated overnight with supernatant from IPTG-induced cultures from phage infected bacteria. Fab production was detected by α-Fab ELISA. Fab binding to HUVECs was detected by α-Fab-AFOS ELISA.

FIG. 8 shows the results of Fab clone binding to HUVECs using an α-KS phage library. Clone #16 appeared to bind well to HUVECs *in vitro*.

These results confirm the utility of using Fab antibody fragments for production of phage display libraries. Such libraries should be enriched in peptide sequences targeted against the specific organ, tissue or cell type used to immunize the host animal, compared to the random sequence phage display libraries that have been used in

previous biopanning methods. The results also confirm the utility of the BRASIL method for identifying targeting peptide sequences.

Example 6. Identification of Receptor/Ligand Pairs: Targeting Peptides against Integrin Receptors

Certain embodiments of the present invention concern the identification of receptor/ligand pairs for various applications. Targeting peptides selective for organs, tissues or cell types bind to receptors (as defined above), normally located on the lumenal surface of blood vessels within the target. In certain embodiments, targeting peptides may be used to identify or characterize such receptors, either directly or indirectly. In addition to their use as targets for delivery of gene therapy vectors, other therapeutic agents or imaging agents for *in vivo* imaging, such naturally occuring receptors are of use as potential targets for development of new therapeutic agents directed against the receptor itself, for development of vaccines directed against the receptor, and for understanding the molecular mechanisms underlying various disease states. Naturally, the targeting peptides themselves may serve as the basis for new therapeutic agents directed against the receptors.

Targeting peptides may frequently act as mimeotopes of endogenous ligands that bind to the targeted receptor. In other embodiments, the endogenous ligands may be identified and characterized using the disclosed methods. Such ligands are also of potential use as targets for development of new therapeutic agents, *etc.*

The present example illustrates one embodiment related to identification of receptor/ligand pairs, in this case, integrin receptors. Non-limiting examples of applications of targeting peptides directed against integrins include regulation of cell proliferation and chemotaxis, pro-apoptosis and anti-angiogenesis. In this embodiment, purified integrins attached to a solid substrate were used to screen phage display libraries to identify targeting peptides directed against integrins.

Background

Integrin function is regulated by cytokines and other soluble factors in a variety of biological systems. Most commonly, exposure to such factors leads to conformational alterations that result in changes in the activation state of the receptors (i.e., increased or decreased affinity for a given ligand and/or receptor clustering in the plasma membrane). Changes in integrin-dependent adhesion ultimately activate various complex signal transduction pathways. At the molecular level, the induced co-localization of cytoskeleton proteins with integrin cytoplasmic domains controls signal transduction.

Cytoplasmic domains are key regulators of integrin function (reviewed in Hynes, 1992; Ruoslahti, 1996). Individual α and ß subunit cytoplasmic domains are highly conserved among different species (Hemler *et al.*, 1994). Although the cytoplasmic domains of various ß subunits share similar primary structures, they differ in certain functional characteristics. Experiments with chimeric integrins have shown that the cytoplasmic domains of ß chains are responsible for regulating receptor distribution and recruitment to focal adhesion sites (Pasqualini and Hemler, 1994). Thus, certain cytoplasmic domains are critical for integrin-mediated signaling into the cell (outside-in signaling) and activation of integrin-ligand binding activity (inside-out signaling) (Hemler *et al.*, 1994).

The integrins αvß3 and αvß5 are selectively expressed in angiogenic vasculature but not in normal vasculature (Brooks *et al.*, 1994a, 1994b; Pasqualini *et al.*, 1997; Arap *et al.*, 1998). Moreover, αv integrin antagonists have been shown to block the growth of neovessels (Brooks *et al.*, 1994a, 1994b, 1995; Hammes *et al.*, 1996). In these experiments, endothelial cell apoptosis was identified as the mechanism for the inhibition of angiogenesis (Brooks *et al.*, 1994a, 1994b, 1995). Angiogenesis initiated by bFGF can be inhibited by an anti-αvß3 blocking antibody, whereas VEGF-mediated angiogenesis can be prevented by a blocking antibody against αvß5. The integrins αvß3 and αvß5 have been reported to be preferentially displayed in different

types of ocular neovascular disease (Friedlander *et al.*, 1995, 1996). Thus, distinct cytokine-induced pathways that lead to angiogenesis seem to depend on specific αv integrins.

Although both αvß3 and αvß5 integrins bind to vitronectin, they probably mediate different post-ligand binding events. For instance, in the absence of exogenous soluble factors, the integrin αvß5 fails to promote cell adhesion, spreading, migration, and angiogenesis. On the other hand, the αvß3 integrin can induce such events without additional stimulation by cytokines (Klemke *et al.*, 1994; Lewis *et al.*, 1996; Friedlander *et al.*, 1995).

Experiments designed to study the molecular basis for cytokine regulation of αvß5 function have shown that upon binding to immobilized vitronectin, inactivated αvß5 is barely detectable in association with actin, α-actinin, talin, tensin, $p130^{cas}$, and vinculin. In contrast, αvß3 induces the localized accumulation of such molecules. Upon activation of protein kinase C (PKC), αvß5 behaves similarly to αvß3, but cannot recruit talin (Lewis *et al.*, 1996). Furthermore, calphostin C, an inhibitor of PKC, seems to block angiogenesis mediated by αvß5 but not by αvß3 (Friedlander *et al.*, 1995). These observations suggest that PKC activation probably affects the conformation or phosphorylation state of the ß5 cytoplasmic domain. Similar changes may occur in cytoplasmic proteins as well (Kolanus and Seed, 1997). The cytokine regulation of αvß5 integrin is unusual because ligand binding is unchanged, but the events that follow ligand binding differ (Lewis et al., 1996). Therefore, cellular events mediated by αvß3 or αvß5 are clearly controlled by different mechanisms (Filardo and Cheresh, 1994b).

The search for αv integrin-associated molecules has been hampered by technical difficulties. First, the physical associations involved are likely to rely on an assembly of multimeric ligands that no longer occurs when cells are not intact. Second, their association to integrins is usually of low affinity. Finally, changes in the conformation

and phosphorylation states of the associating proteins may add a further level of complexity in these transiently modulated interactions. Because of these problems, only a limited number of proteins that bind to integrin cytoplasmic domains have been identified. These proteins, such as paxillin and ICAP-1, mainly associate with the ß1 chain (Shattil and Ginsberg, 1997). Cytohesin-1 and filamin associate with the cytoplasmic domain of ß2.

Several other proteins reportedly interact with ß integrin cytoplasmic domains in general: talin, filamin, α-actinin, focal adhesion kinase, the serine/threonine kinase ILK, and skelemin. Talin, α-actinin, and focal adhesion kinase no longer co-localize with ß1 integrins after deletion of their putative binding sites in the ß1 cytoplasmic domain. Similar approaches have shown that other cytoskeleton-associated proteins and signaling molecules co-localize with integrins.

Integrins associate with molecules that are involved in growth factor signaling. In addition to the 190-kDa protein and IRS-1, which can be found in association with αvß3 (Vuori and Ruoslahti, 1994), analysis of the association of the αvß3 integrin with molecules related to the insulin and PDGF signaling pathways revealed that both the insulin and PDGFß receptors co-immunoprecipitate with αvß3. The receptor molecules associated with the integrin represent a highly phosphorylated and highly activated subfraction of such molecules. These results are important because they reinforce the notion that integrin-mediated cell attachment coordinates cellular responses to growth factors. Integrin-dependent signaling processes synergize with proliferation signals (Frisch and Ruoslahti, 1997; Clark and Brugge, 1995; Longhurst and Jennings, 1998).

Protein phosphorylation is one of the earliest events detected in response to integrin stimulation. The ability of tyrosine kinase inhibitors to obstruct the formation of focal adhesions suggests a role for tyrosine phosphorylation in the signaling pathways linked to integrin receptors (Defilippi et al., 1994). Serine/threonine kinase families, such as protein kinase C (PKC) and mitogen-activated protein (MAP) kinase, are also activated upon integrin stimulation, and inhibitors of PKC block cell

attachment and spreading in certain cell systems (Vuori and Ruoslahti, 1993). Integrins seem to affect cell survival by regulating programmed cell death, a response that also depends on tyrosine phosphorylation. Several proteins that associate with integrin protein complexes contain modular domains, termed Src homology 2 (SH2) and 3 (SH3), that specifically mediate protein-protein coupling. SH2 domains bind to proteins through interactions with specific peptide motifs containing phosphotyrosine, whereas SH3 domains bind to short proline-rich peptide motifs on their protein targets (Clark and Brugge, 1995). Integrin-mediated cell adhesion causes activation of MAP kinases and increased tyrosine phosphorylation of focal adhesion kinase (FAK). Autophosphorylation of FAK leads to the binding of SH2-domain proteins including Src-family kinases and the Grb-2-Sos complex. One plausible hypothesis is that integrin-mediated tyrosine phosphorylation of FAK leads to activation of the Ras cascade and ultimately to MAP kinase activation. However, integrin-mediated MAP kinase activation has been shown to be independent of FAK, indicating that at least two distinct integrin signaling pathways might exist: (i) MAP kinase activation, which may play a role in mitogenic and survival signals, and (ii) FAK tyrosine phosphorylation, which is clearly involved in cytoskeletal organization (Lin et al., 1997).

Previous studies of peptidic substrates and homology-based molecular models suggested that about 9–13 residues of a peptidic substrate contact the active-site cleft of the kinase domain (Bossemeyer et al., 1993). The phage display technique offers an alternative approach to generating and selecting diverse combinatorial-peptide libraries (Smith, 1991; Wells and Lowman, 1992). Because the chemical diversity in a phage display library is encoded by DNA that can be replicated and amplified, selection of a phage library can be performed over multiple rounds, allowing even rare motifs to be identified. In contrast to synthetic chemical libraries, phage display permits the analysis of single species instead of pooled species. The power of this technique has been demonstrated mainly through the selection of rare antibodies or peptides from large combinatorial libraries.

A combinatorial phage library has been used for determining the preferred substrate sequences for different protein-tyrosine kinases (PTKs), all of them closely related members of the Src family and one more distantly related PTK, Syk (Schmitz et al., 1996). Subsequent phosphorylation by recombinant PTKs and selection of phosphorylated phage by an anti-phosphotyrosine antibody were used to enrich for phage that displayed substrate peptides. After several rounds of selection, distinct substrate sequences were found for each of the PTKs tested. For the PTKs related to the Src family, critical features of these canonical sequences were recapitulated in known or presumed protein substrates. Most notably, amino acids directly flanking the invariant tyrosine residue were found to be highly conserved and specific for each of the PTKs tested. The identified motifs could, therefore, provide a rational basis for developing small and specific inhibitors of the catalytic domain of PTKs (Schmitz et al., 1996).

Further studies extended the scope of phage display technology by showing how peptide libraries can be used to investigate the substrate specificity of Fyn, a protein kinase of the Src family (Dente et al., 1997; Gram et al., 1997). Modified peptides displayed by phage were used to determine the phosphotyrosine specificity of the phosphotyrosine-binding domain (PTB) of the protein Shc (Dente et al., 1997). Other related experiments focused on identifying phosphopeptide ligands that interact with the Src homology 2 (SH2) domain of the adapter protein Grb2 by screening a random peptide library established on phage. Phage were phosphorylated *in vitro* at an invariant tyrosine residue by a mixture of the phosphotyrosine kinases c-Src, Blk, and Syk. Binding motifs were selected by interaction of the library with the recombinant SH2 domain of Grb2 expressed as a glutathione-S-transferase (GST) fusion protein. Several subsequent cycles of selection led to the enrichment of phage that bound to the GST-Grb2 SH2 domain only when previously phosphorylated. Sequence analysis revealed that all of the selected phage displayed peptides with the consensus motif Y*M/NW (Y* denotes phosphotyrosine). One peptide bound the Grb2 SH2 domain with 3-fold higher affinity than the peptide motif Y*VNV, which is derived from the

natural ligand Shc. These findings show that phage display can be used to rapidly identify high-affinity ligands to SH2 domains and other interacting proteins involved in signal transduction.

The cytoplasmic domain of ß5 is structurally and functionally unique with regard to other integrin subunits (Table 8) and shares only 38% homology to the cytoplasmic domain of ß3 (Hemler et al., 1994). It has been proposed that the structural requirements for association with αv prevented further primary sequence divergence between ß3 and ß5; yet the existing differences are likely to account for the reduced interaction of αvß5 with talin (Lewis et al., 1996). The cytoplasmic domain of ß5, when expressed in Chinese hamster ovary (CHO) cells as a chimera with the extracellular domain of ß1, led the chimeric receptor to behave like ß5, promoting cell migration and loss of receptor localization to focal adhesions (Pasqualini and Hemler, 1994). The cytoplasmic domains of integrin ß1 and ß3 subunits, however, were shown to be functionally interchangeable (Solowska *et al.*, 1991). Other studies have shown that αvß3 and αvß5 seem to differ in terms of localization to focal adhesion and their contribution to cell migration (Delannet et al., 1994; Filardo et al., 1995). However, these reported functional divergences have not been mapped to specific domains.

Table 8. Alignment of similar integrin ß subunit cytoplasmic domains. The main differences between the ß3 and ß5 cytoplasmic are highlighted.

ß1	HDRREFAKFEKEKMNAKWDTGENPIYKSAVTTVVNPKYEGK
ß2	SDLREYRRFEKEKLKSQWNN-DNPLFKSATTTVMNPKFAES
ß3	HDRKEFAKFEEERARAKWDTANNPLYKEATSTFTNITYRG
ß5	HDRREFAKFQSERSRARYEMASNPLYRKPISTHTVDFTFNKSYNGTVD

After the angiogenesis switch is triggered, distinct molecules are likely to associate with either ß3 or ß5. Moreover, selective associations with the αv

cytoplasmic domain may also be possible, in the context of each of the heterodimers. For example, a ß turn in the cytoplasmic tail of the integrin αv subunit has been shown to influence conformation and ligand binding of αvß3 (Filardo and Cheresh, 1994). The basis of selective signaling properties may be the assembly of specific molecules that associate with the respective cytoplasmic domains. The present study defines the molecules involved in αvß3- and αvß5-selective angiogenic signaling by exploring a novel strategy, panning of phage display peptide libraries on ß3 and ß5 cytoplasmic domains and determining the biological properties of the cytoplasmic domain-binding peptides.

The disclosed methods have several advantages over previous approaches: (i) the ability to characterize the intracellular molecules that directly or indirectly interact with integrin cytoplasmic domains; (ii) the development of antibodies against molecules that bind to integrin cytoplasmic domains in very low amounts; and (iii) the phage display library screenings will lead to the identification of peptides that mimic cytoplasmic-domain binding proteins.

Methods

Two dimensional cell culture

Three human endothelial cell lines that express ß3 and ß5 integrins were used: KS1767 cells (Herndier *et al.*, 1996), HUVECs (ATCC), and BCE cells (Solowska *et al.*, 1991). Sterile glass coverslips covered with different proteins (i.e. vitronectin, fibronectin, collagen, or laminin) were used as substrates. After cells attached and spread, the monolayers were rendered quiescent by a 12-hour incubation in medium containing 0.05% fetal calf serum. Peptides were introduced into the cells using the penetratin membrane-permeable tag (see below). The cells were plated onto ECM proteins for adhesion and spreading. The monolayer was stimulated for 6 hours with each of the growth factors involved in αv-mediated angiogenesis, including bFGF, TNFα, VEGF, and TGFβ. Untreated cells were the negative controls.

Three-Dimensional Cell Culture:

150 µl of Matrigel were added per well of 24-well tissue culture plates and allowed to gel at 37°C for 10 min. HUVECs starved for 24 h in M199 medium supplemented with 2% FCS before being trypsinized were used. 10^4 cells were gently added to each of the triplicate wells and allowed to adhere to the gel coating for 30 min at 37°C. Then, medium was replaced with peptides in complete medium. The plates were monitored and photographed after 24 h with an inverted microscope (Canon).

Chemotaxis Assay:

Cell migration assays were performed as follows: 48-well microchemotaxis chambers were used. Polyvinylpyrrolidone-free polycarbonate filters (Nucleopore, Cambridge, MA) with 8-µm pores were coated with 1% gelatin for 10 min at room temperature and equilibrated in M199 medium supplemented with 2% FCS. Peptides were placed in the lower compartment of a Boyden chamber in M199 supplemented with 2% FCS, 20 ng/ml VEGF-A (R&D System), and 1 U/ml heparin. Overnight-starved subconfluent cultures were quickly trypsinized, and resuspended in M199 containing 2% FCS at a final concentration of 2×10^6 cells/ml. After the filter was placed between lower and upper chambers, 50 µl of the cell suspension was seeded in the upper compartment. Cells were allowed to migrate for 5 h at 37°C in a humidified atmosphere with 5% CO_2. The filter was then removed, and cells on the upper side were scraped with a rubber policeman. Migrated cells were fixed in methanol and stained with Giemsa solution (Diff-Quick, Baxter Diagnostics, Rome, Italy). Five random high-power fields (magnitude 40×) were counted in each well.

Proliferation Assay:

Cell proliferation was measured as described (Pasqualini and Hemler, 1994). Briefly, 4×10^4 HUVECs were incubated in 24-wells plates. The cells were starved for 24 h, and then the medium was removed and replaced in the presence of VEGF and 15 µM of each peptide and incubated for 18 h. Then, 50 µl of media containing

[^{3}H]thymidine (1 μCi/ml) was added to the wells, and after 6 additional hours of incubation at 37°C, the medium was removed and the cells were fixed in 10% TCA for 30 min at 4°C, washed with ethanol, and solubilized in 0.5 N NaOH. Radioactivity was counted by liquid scintillation with an LS 6000SC Beckman scintillation counter. Each experiment was performed three times with triplicates, and the results are expressed as the mean ± SD.

Apoptosis Assay (propidium iodide staining subdiploid population)

Approximately 1 x 10^6 cells were harvested in complete media and 15 μM of peptide added for 4, 8, or 12 h. The cells were then washed in PBS and resuspended in 0.5 ml propidium iodide solution (50μg/ml PI, 0.1% Triton X-100, 0.1% sodium citrate). After a 24-h incubation at 4°C, cells were counted with a XL Coulter (Coulter Corporation) with a 488-nm laser; 12,000 cells were counted for each histogram, and cell cycle distributions were analyzed with Multicycle program.

After microinjection or penetratin-mediated internalization of the peptides and appropriate controls, cell apoptosis was monitored using the ApopTag kit. Experiments were performed in the presence of caspase inhibitors and antibodies against specific caspases.

Cytokine- and Tumor-Induced Angiogenesis Assays

Angiogenic factors and tumor cells implanted into CAM stimulate growth of new capillaries. Angiogenesis was induced in CAMs from 10-day chicken embryos by VEGF or bFGF filters implanted in regions that were previously avascular. Different treatments (penetratin peptides and controls) were applied topically, and after 3 days, the filters and surrounding CAMs were resected and fixed in formalin. The number of blood vessels entering the disk was quantified within the focal plane of the CAM with a stereomicroscope. The mean number of vessels and standard errors from 8 CAMs in each group were compared.

Phosphorylation and panning of phosphorylated phage libraries:

Phosphorylation of peptide libraries with src family protein kinases (Fyn, c-Src, Lyn, and Syc) and serine/threonine kinases such as a MAP kinase were performed as described previously (Schmitz et al., 1996; Dente et al., 1997; Gram et al., 1997). Briefly, phage particles were collected from culture supernatants by double precipitation with 20% polyethylene glycol 8000 in 2.5 M NaCl. Particles were dissolved at 10^{12} particles/ml. Purified phage (10 μl) were incubated for 3 hours at room temperature with different concentrations (35 to 3,500 units) of protein kinases in a reaction buffer volume of 50 μl. The reaction mixtures were transferred to tubes containing 10 μg of agarose-conjugated anti-P-Tyr, anti-P-Ser, or anti-P-Thr monoclonal antibodies to select phage displaying phosphorylated peptides. Bound phage were eluted by washing the column with 0.3 ml of elution buffer (0.1 M NaCl/glycine/1 mg/ml BSA, pH 2.35). The eluates were neutralized with 2 M Tris-base and incubated with 2 ml of a mid-log bacteria culture. Aliquots of 20 μl were removed for plating, and phage were harvested as described. The phosphorylation-selection step was repeated. Phosphorylated peptides binding to ß3 and ß5 cytoplasmic domains were analyzed as described in the previous section.

Matrix-assisted laser desorption time-of-flight (MALDI-TOF) mass spectrometry was used to map *in vitro* phosphorylation sites on the β3 and β5 cytoplasmic domains and cytoplasmic domain-binding peptides. The fusion proteins or peptides were phosphorylated *in vitro* as described and purified by RP-HPLC or RP microtip columns. Phosphorylated peptides were identified by three methods: (1) 80-Da mass shifts after kinase reactions; (2) loss of 80 Da after phosphatase treatment; or (3) loss of 80 Da or 98 Da in reflector vs. linear mode for tyrosine phosphorylated or serine, threonine phosphorylated peptides, respectively. Where needed, peptides were purified by RP-HPLC and subjected to carboxypeptidase and aminopeptidase digestions to produce sequence ladders. This was particularly useful where one peptide may harbor two or more phosphorylation sites.

Panning on phosphorylated GST- fusion proteins.

GST fusion proteins were phosphorylated *in vitro* as described (Schmitz et al., 1996; Dente et al., 1997; Gram et al., 1997). Briefly, 10 μg/ml was incubated for 3 h at room temperature with 5.5 units of Fyn protein kinase in reaction buffer (50 mM Tris, 5mM $MgCl_2$, 500 μM Na_3VO_4, 500 μM ATP in a total volume of 50 μl). The reaction was stopped by adding 40% of TCA. After the kinase substrate protein was precipitated, it was resuspended in PBS and coated on microtiter wells at 10 μg/well. An aliquot of CX7C library ($2.5x10^{11}$ transducing units was incubated on the GST fusion proteins. Phage were sequenced from randomly selected clones.

Mass Spectrometry Studies

Mass spectrometric peptide mass mapping was used to identify novel ligands for ß3 and/or ß5 cytoplasmic domains. Polyclonal and monoclonal antibodies raised against the cytoplasmic domain-binding peptides were used to purify target proteins (cytoskeletal or signaling molecules). These proteins were resolved by SDS-PAGE, cut out from the SDS gels, and digested in-gel with trypsin. After extraction of the peptides, MALDI-TOF mass spectrometry analysis was performed to produce a list of peptide masses. This list of peptide masses, in combination with protease specificity, produces a relatively specific "signature" that can be used to search sequence databases. If the protein sequence is present in a database, the protein can be identified with high confidence by this method. The lower detection limit for this approach is currently 1 pmol, at least 10–20- fold better than N-terminal Edman sequencing methods.

Results

Panning of phage peptide libraries on ß3 or ß5 cytoplasmic domains.

ß3 and ß5 cytoplasmic domain-binding peptides were isolated by screening multiple phage libraries with recombinant GST fusion proteins that contained either GST-β3cyto or GST-ß5cyto coated onto microtiter wells. Immobilized GST was used as a negative control for enrichment during the panning of each cytoplasmic domain.

Phage were sequenced from randomly selected clones after three rounds of panning as disclosed elsewhere (Koivunen *et al.*, 1995; Pasqualini *et al.*, 1995). Distinct sequences were isolated that interacted specifically with the ß3 or with the ß5 cytoplasmic domains (Table 9). Randomly selected clones from panning rounds II and III were sequenced. Amino acid sequences of the phagemid encoded peptides were deduced from nucleotide sequences. The most frequent motifs found after panning with the indicated libraries are shown in Table 9. The ratios were calculated by dividing the number of colonies recovered from β3-GST-coated wells and those recovered from GST or BSA.

Table 9. Sequences displayed by phage binding to ß3 or β5 integrin cytoplasmic domain

Peptide motif	**SEQ ID NO**	**β3/GST Ratio**	**β3/BSA Ratio**
CX_9 Library			
CEQRQTQEGC	SEQ ID NO:93	4.3	14
CARLEVLLPC	SEQ ID NO:94	2.8	18.7
X_4YX_4 Library			
YDWWYPWSW	SEQ ID NO:95	5.6	163
GLDTYRGSP	SEQ ID NO:96	4.1	48
SDNRYIGSW	SEQ ID NO:97	3.3	32
YEWWYWSWA	SEQ ID NO:98	2.2	28.1
KVSWYLDNG	SEQ ID NO:99	2.1	20
SDWYYPWSW	SEQ ID NO:100	2.1	157
AGWLYMSWK	SEQ ID NO:101	1.8	2.4
Pool Cyclic Libraries			

CFQNRC	SEQ ID NO:102	3.1	16
CNLSSEQC	SEQ ID NO:103	2.7	62
CLRQSYSYNC	SEQ ID NO:104	2.4	3.2
Peptide motif	**SEQ ID NO**	**β5/GST Ratio**	**β5/BSA Ratio**
Pool Cyclic Libraries			
CYIWPDSGLC	SEQ ID NO:105	5.2	193
CEPYWDGWFC	SEQ ID NO:106	3.1	400
CKEDGWLMTC	SEQ ID NO:107	2.3	836
CKLWQEDGY	SEQ ID NO:108	1.8	665
CWDQNYLDDC	SEQ ID NO:109	1.5	100
X_4YX_4 Library			
DEEGYYMMR	SEQ ID NO:110	11.5	29
KQFSYRYLL	SEQ ID NO:111	4.5	8
VVISYSMPD	SEQ ID NO:112	3.8	28
SDWYYPWSW	SEQ ID NO:113	2.4	304
DWFSYYEL	SEQ ID NO:114	1.7	153

The specificity of the interaction with ß3 or ß5 cytoplasmic domains was determined by calculating the ratios between the number of phage bound to the cytoplasmic domain containing-fusion proteins (ß3 or ß5) versus GST alone (negative control). FIG. 9 shows the results from binding assays performed with the GST-ß3cyto binding phage. Six phage were tested that displayed the motifs most frequently found during the second and third rounds of panning. Each panel shows the results from binding assays for the phage displaying different peptides that bind to the ß3 cytoplasmic domain, as indicated. Insertless phage or unselected libraries were used as

negative controls and did not show binding above background. Two plating dilutions were shown for each assay.

A similar strategy was used to determine the specificity of the phage isolated in the screenings involving the ß5 cytoplasmic domain fusion protein. The binding assays were performed with individually amplified phage, shown in FIG. 10. Five phage were tested that displayed the motifs found most frequently during the second and third rounds of panning. Each panel shows the binding assays for the phage displaying peptides that bind to the ß5 cytoplasmic domain. Insertless phage or unselected libraries were used as negative controls and did not show binding above background in these assays.

To determine whether the binding of the selected motifs was specific for each cytoplasmic domain, binding assays were performed comparing the interaction of individual phage motifs with ß1, ß3, or ß5 cytoplasmic domain fusion proteins. ELISA with anti-GST antibodies showed that the three proteins can be coated onto plastic at equivalent efficiency, and thus the differences in binding do not reflect differences in coating concentrations (not shown). Both the ß3- and ß5-selected phage selectively interacted with the proteins on which they were originally selected, with average binding selectivities observed of $\beta3/\beta1 = 3.9$, $\beta3/\beta5 = 3.7$, $\beta5/\beta1 = 4.8$, and $\beta5/\beta3 = 6.9$ (not shown). The average selectivity for integrin cytoplasmic domains versus BSA was about one to two orders of magnitude (not shown). None of the phage tested seemed to bind strongly to the ß1 cytoplasmic domain (not shown).

Characterization of synthetic peptides corresponding to the sequences displayed by the integrin-cytoplasmic domain-binding phage.

Specific phage were selected for further studies on the basis of their binding properties. Synthetic peptides corresponding to the sequence displayed by each phage were used to perform binding inhibition studies. This assay determined whether phage binding was entirely mediated by the targeting peptide displayed by the phage or whether it also included a non-specific component. As expected, the synthetic peptides inhibited the binding of the corresponding phage in a dose-dependent manner (FIG. 11

and FIG. 12). A control peptide containing unrelated amino acids had no effect on phage binding when tested at identical concentrations.

Phosphorylation events modulate the interaction of the selected peptides with cytoplasmic domains

Events involving phosphorylation are important in regulating signal transduction. The phage display system was used to evaluate the effect of tyrosine phosphorylation at two levels. First, recombinant fusion proteins containing ß3 or ß5 cytoplasmic domains were used for panning of phage libraries displaying tyrosine-containing peptides. Second, the cytoplasmic domains themselves were phosphorylated before phage selection was performed. Experiments were performed to investigate the capacity of specific tyrosine kinases to modulate the interaction of the selected peptides with the cytoplasmic domains. The results obtained in the panning of phage libraries displaying tyrosine-containing peptides are shown in Table 10.

Randomly selected clones from rounds III and IV were sequenced from a X4YX4 phosphorylated library with Fyn. Amino acid sequences of the phagemid encoded peptides were deduced from nucleotide sequences. Table 10 shows the motifs found most frequently after the indicated libraries were panned with β3 or β5. The ratio of binding to β3 or β5 was calculated by dividing the number of β3 or β5 colonies by GST or BSA colonies found after panning. The ratio of binding to ß3 or ß5 with phosphorylated phage by Fyn versus unphosphorylated phage was calculated by dividing the number of colonies found after the panning.

Table 10. Sequences displayed by phosphorylated phage binding to integrin cytoplasmic domains.

Peptide Motif		**Phos/Unphos**	**β3 or β5/GST**	**β3 or β5/BSA**
<u>β3 cytoplasmic</u>				
GGGSYRHVE	SEQ ID NO:115	13.2	1.5	5.3
RAILYRLAN		2.8	1.3	20
MLLGYRFEK	SEQ ID NO:116	2.5	3.5	2.7

	SEQ ID NO:117			
ß5 cytoplasmic				
TMLRYTVRL	SEQ ID NO:118	14.3	3.4	2.2
TMLRYFMFP	SEQ ID NO:119	4.2	2.3	3.8
TLRKYFHSS	SEQ ID NO:120	3.8	3.8	15.2
TLRKYFHSS	SEQ ID NO:121	1.8	5.6	7.3

The effect of phosphorylation on the affinity and specificity of the cytoplasmic domain-binding was examined. Phage displaying the ß3 and ß5 cytoplasmic domain-binding peptides were phosphorylated *in vitro* as previously described (Schmitz et al., 1996; Dente et al., 1997; Gram et al., 1997), using Fyn kinase. Specific phosphorylation of the tyrosine-containing peptide on the surface of the phage was confirmed by using ^{32}P-gamma dATP in the kinase reaction and by separating the phage pIII protein by SDS-PAGE.

Phage phosphorylated *in vitro* showed increased binding affinity and specificity to the ß3 integrin cytoplasmic domain (FIG. 13). The TLRKYFHSS (SEQ ID NO:120) phage was also tested in assays that included other GST-cytoplasmic domain fusion proteins to determine specificity (FIG. 14).

Sequence similarity of integrin binding peptides with known cytoskeletal and signaling proteins.

The peptides displayed by integrin cytoplasmic domain-binding phage were similar to certain regions found within cytoskeletal proteins and proteins involved in signal transduction (Table 11). The similarity of some of the isolated peptides to a region of mitogen-activated protein kinase 5 (MAPK5, amino acids 227–234) was particularly interesting. A connection involving the MAPK cascade, cell adhesion, migration and proliferation has been proposed (Lin et al., 1997)

Table 11. Sequence similarity of integrin binding peptides with known cytoskeletal and signaling proteins.

Isolated Motif	Candidate Proteins	Region (AA #)	Homology %
β3 cytoplasmic			
GLDTYRGSP	Ras-related protein	124-133	75
(SEQ ID NO:96)	Ser/Thr kinase (K-11)	18-25	75
SDNRYIGSW	PDGF receptor	985-992	85
(SEQ ID NO:97)	Phosphatidylinositol 4 phosphatase 5	233-241	85
		185-191	85
	Receptor protein kinase	71-79	63
CEQRQTQEGC	Protein kinase clk2	227-234	75
(SEQ ID NO:93)	MAPK5	494-503	78
CLRQSYSYNC	Phophatidylinositol 3-kinase	230-239	75
(SEQ ID NO:104)	Cyclin-dependent kinase 5 (cdk5)		
β5 cytoplasmic			
VVISYSMPD	Ser/Thr kinase	479-485	83
(SEQ ID NO:112)	IFN (β chain)	27-35	70
	Actin	240-248	67
	Focal adhesion kinase	43-51	75
DEEGYYMMR	Tubulin	60-66	100
(SEQ ID NO:110)	Putative Ser/Thr kinase	292-299	86

Membrane-permeable peptides

Penetratin is a peptide that can translocate hydrophilic compounds across the plasma membrane. Fusion to the penetrating moiety allows oligopeptides to be targeted directly to the cytoplasm, nucleus, or both without apparent degradation (Derossi et al., 1994). This membrane-permeable peptide consists of 16 residues

(RQIKIWFQNRRMKWKK, SEQ ID NO:122) corresponding to amino acids 43–58 of the homeodomain of Antennapedia, a Drosophila transcription factor (Joliet et al., 1991a, 1991b; Le Roux et al., 1993). Internalization mediated by penetratin occurs at both 37°C and 4°C, and the internalized peptide can be retrieved intact from cells.

Peptides were designed containing penetratin sequences fused to the sequences of motifs found to bind ß3 or ß5 cytoplasmic domains. The peptides were synthesized on a 431 Applied Biosystems peptide synthesizer using p-hydroxymethylphenoxy methyl polystyrene (HMP) resin and standard Fmoc chemistry. Peptide internalization and visualization was performed as described (Derossi et al., 1994; Hall et al., 1996; Theodore et al., 1995).

Briefly, 10–50 μg/ml of the biotinylated peptide was added to cells in culture. Peptides were incubated with plated cells. After 2–4 hours, the cultures were washed three times with tissue culture media, fixed and permeabilized using ethanol:acetic acid (9:1) for 5 min at –20°C. Nonspecific protein binding sites were blocked by incubating the cultures for 30 min with Tris-buffered saline (TBS) containing 10% fetal calf serum (FCS) and 0.02% Tween. The cultures were incubated in the same buffer containing FITC-conjugated Streptavidin (1:200 dilution) and washed with TBS before being mounted for viewing by confocal microscopy. The penetratin-linked peptides were internalized quite efficiently (data not shown).

Functional data showed that the cytoplasmic domain-binding peptides selected on β3 or β5 can interfere with integrin-mediated signaling and subsequent cellular responses (i.e., endothelial cell adhesion, spreading, proliferation, migration). A commercial panel of "internalizable" versions of the synthetic motifs found by phage screenings (SDNRYIGSW, SEQ ID NO:97; and CEQRQTQEGC, SEQ ID NO:93; ß3 binding peptides and VVISYSMPD, SEQ ID NO:112; a ß5-binding peptide) were obtained. These complex chimeric peptides consist of the most selective of the β3 or β5-cytoplasmic domain-binding peptides coupled to penetratin, plus a biotin moiety to allow the peptides to be tracked once they were internalized into intact cells. These

membrane-permeable forms of the peptides are internalized, may affect β3 and β5 post-ligand binding cellular events and can induce massive apoptosis (data not shown).

Endothelial cell proliferation, chemotaxis and apoptosis

The effect of ß3 and ß5 integrin cytoplasmic domain-binding motifs on endothelial cell proliferation was evaluated after stimulation with factors that activate endothelial cells (FIG. 15). Cell proliferation was measured according to Pasqualini and Hemler (1994). Briefly, $4x10^4$ HUVECs were incubated in 24-well plates and starved for 24 h, after which the medium was removed and replaced in the presence of VEGF and 15 μM of each peptide. After another 18 h of incubation, 50 μl of medium containing [^{3}H]thymidine (1μCi/ml) was added to the wells. After 6 additional hours of incubation at 37^{0}C, the medium was removed and the cells were fixed in 10% TCA for 30 min at 4°C, washed with ethanol and solubilized in 0.5 N NaOH. Radioactivity was counted by liquid scintillation by using a LS 6000SC Beckman scintillation counter. Each experiment was performed three times with triplicates, and the results were expressed as the mean ± SD.

The effect of ß3 and ß5 integrin cytoplasmic domain-binding motifs in endothelial cell migration was evaluated after stimulation with factors that activate endothelial cells. The peptides tested affected cell function in a dose-dependent and specific way. Their properties seem to be intrinsic to the ß3 or to the ß5 cytoplasmic domain (FIG. 16).

Chemotaxis Assay.

Cell migration was assayed in a 48-well microchemotaxis chamber. Polyvinylpyrrolidone-free polycarbonate filters with 8-μm pores were coated with 1% gelatin for 10 min at room temperature and equilibrated in M199 medium supplemented with 2% FCS. Peptides were placed in the lower compartment of a Boyden chamber in M199 supplemented with 2% FCS, 20 ng/ml VEGF-A (R&D System), and 1 U/ml heparin. Overnight-starved subconfluent cultures were quickly trypsinized, and resuspended in M199 containing 2% FCS at a final concentration of

2×10^6 cells/ml. After the filter was placed between lower and upper chambers, 50 µl of the cell suspension was seeded in the upper compartment. Cells were allowed to migrate for 5 h at 37°C in a humidified atmosphere with 5% CO_2. The filter was then removed, and cells on the upper side were scraped with a rubber policeman. Migrated cells were fixed in methanol and stained with Giemsa solution. Five random high-power fields (magnitude 40×) were counted in each well. The results show that both β3-integrin cytoplasmic domain binding peptides increased cell migration but penetratin did not affect the cells.

Apoptosis assay (Propidium Iodide (PI) staining subdiploid population).

Approximately $1x10^6$ cells were harvested in complete medium, and 15 µM of peptide was added for 4, 8, or 12 hours. The cells were then washed in PBS and resuspended in 0.5 ml propidium iodide solution (50 µg/ml PI, 0.1% Triton X-100, 0.1% sodium citrate). After a 24-h incubation at 4°C, the cells were counted with an XL Coulter (Coulter Corporation) with a 488 nm laser; 12,000 cells were counted for each histogram, and cell cycle distributions were analyzed with the Multicycle program.

Treatment of cells with VISY-penetratin chimera resulted in induction of apoptosis (FIG. 17, panel d) Pro-apoptotic effects were not observed when the cells were exposed to other growth factors (not shown). Penetratin alone and the other penetratin chimeras also could not induce similar effects (FIG. 17, panel c). This finding shows that novel approaches for inhibiting angiogenesis can be developed based on the use of integrin targeting peptides.

Immunization with cytoplasmic domain binding peptides and characterization of the resulting antibodies

Polyclonal antibodies that recognize αvß3 and αvß5-binding peptides were generated using KLH conjugates made with the synthetic peptides, according to standard techniques. Antibodies against two different synthetic peptides have been produced (FIG. 18). The sera not only recognize the immobilized peptides, but also

recognize specific proteins in total cell extracts, as shown by western blot analysis (FIG. 19).

Rabbits were immunized with SDNRYIGSW (SEQ ID NO:97) or GLDTYRGSP (SEQ ID NO:96) -KLH conjugates. Each rabbit was injected with 200 μg of peptide conjugated with KLH in Complete Freund's Adjuvant. Between 20 and 60 days later, the rabbits were injected with 100 μg Incomplete Freund's Adjuvant. After the third immunization, sera was collected. Preimmune serum obtained before the first immunization was used as an additional control in the experiments.

The polyclonal antibodies were tested by ELISA, Western blot and immunoprecipitation. In the ELISA assays, microtiter well plates were coated with 10 μg/ml of peptides. The plates were dried at 37°C, blocked with PBS+3% BSA, and incubated with different serum dilutions in PBS+1% BSA. After washing and incubation with the secondary antibody, an alkaline phosphate substrate was added and antibody binding detected colorimetrically at 405 nm. The reactivity observed both in the mouse and rabbit polyclonal sera was highly specific. In all cases, antibody binding could be abrogated by preincubation with the corresponding peptide that was used for immunization, but not by a control peptide (FIG. 18 and FIG. 19). Antibodies raised against two of the β3 cytoplasmic domain binding peptides recognize specific bands on total cell extracts and in immunoprecipitation experiments using 35S-labeled extracts. Similar results were obtained with polyclonal sera and purified IgG's (not shown).

The present example shows that targeting peptides against specific domains of cell receptors can be identified by phage display. Such peptides may be used to identify the endogenous ligands for cell receptors, such as endostatin. In addition, the peptides themselves may have therapeutic effects, or may serve as the basis for identification of more effective therapeutic agents. The endostatin targeting peptides identified herein, when introduced into cells, showed effects on cell proliferation, chemotaxis and apoptosis. The skilled artisan will realize that the present invention is not limited to the disclosed peptides or therapeutic effects. Other cell receptors and ligands, as well as inhibitors or activators thereof, may be identified by the disclosed methods.

Example 7. Induction of Apoptosis with Integrin Binding Peptides (Endothanos)

Example 9 showed that the VISY peptide (VVISYSMPD, SEQ ID NO:112), imported into cells by attachment to penetratin, could induce apoptosis in HUVEC cells. Antibodies raised against the VISY peptide were used to identify the endogenous cell analog of the peptide, identified herein as Annexin V. The results indicate that Annexin V is an endogenous ligand for the integrins that is involved in a novel pathway for apoptosis.

Methods

Protein purification

Polyclonal antibodies against the VISY peptide (VVISYSMPD, SEQ ID NO:112) were prepared using the methods described in Example 9 above. MDA-MB-435 breast carcinoma cells were used for purification of the endogenous VISY peptide analog. Cells were washed three times with ice cold PBS and lysed with chilled water for 20 mn. Cell extracts were centrifuged for 30 min at 100,000 x g to separate the cytoplasmic fraction from the membrane fraction. The cytoplasmic fraction was subjected to column chromatography on a gel filtration column (10-50kDa) and an anion exchange column (mono Q). The anion exchange column was eluted with a salt gradient from 50 mM to 1 M NaCl. One ml fractions were collected, run on SDS-PAGE and tested by Western blotting for the presence of endogenous proteins reactivce with the anti-VISY antibody. The fraction of interest, containing a 36 kDa antibody reactive band, eluted at about 300 mM NaCl.

The 36 kDa always appeared in fractions that showed positive reactivity with the anti-VISY antibody. The fractions were analyzed by SDS-PAGE and 2-D gel electrophoresis, followed by Western blotting. A substantial enrichment of the 36 kDa protein was seen after column chromatography (not shown). The 36 kDa peptide was cut from the SDS-PAGE gel and analyzed by mass spectroscopy to obtain its sequence. All five peptide sequences that were obtained by mass spectroscopy showed 100% homology to the reported sequence of Annexin V (GenBank Accession No.

GI_468888). In addition to its presnece in 435 cells, the 36 kDa band was also seen in Kaposi sarcoma, SKOV and HUVEC cells (not shown).

Commercial antibodies against Annexin V were obtained (Santa Cruz Biologics, Santa Cruz, CA). Comparative Western blots were performed using the anti-VISY antibody and the anti-Annexin V antibody. Both antibodies showed reactivity with the 36 kDa protein (not shown). These results indicate that the endogenous protein analog of the VISY peptide is Annexin V.

Protein-protein interaction with Annexin V and β5 cytoplasmic domain.

Competitive binding assays were performed to examine the binding of Annexin V to β5 integrin and the effect of the VISY peptide. Plates were coated with GST fusion proteins of the cytoplasmic domains of various integrins and Annexin V was added to the plates. Binding of Annexin V was determined using anti-Annexin V antibodies. As shown in FIG. 20A, Annexin V did not bind to either the GST-β1 or GST-β3 integrins. Annexin V bound strongly to the GST-β5 integrin, but binding was dependent on the buffer used (FIG. 20A). Low binding was observed in Tris-buffered saline (TBS), while high binding was observed in "cytoplasmic buffer" (100 mM KCl, 3 mM NaCl, 3.5 mM $MgCl_2$, 10 mM PIPES, 3 mM DTT) with or without added calcium (2 mM) (FIG. 20A). Calcium was used because Annexin V activity has been reported to be modulated by calcium. Binding of Annexin V to GST-β5 was blocked by addition of the VISY peptide (FIG. 20A). FIG. 20B shows the relative levels of binding of anti-Annexin V antibody to purified Annexin V and to VISY peptide.

A reciprocal study was performed, using Annexin V to coat plates and adding GST fusion proteins of integrin cytoplasmic domains. Binding was assessed using anti-GST fusion protein antibodies. As expected, only GST-β5 showed substantial binding to Annexin V, while GST-β1 and GST-β3 showed low levels of Annexin V binding (not shown). In some studies, calcium ion appeared to interfere with the binding interaction between GST-β5 and Annexin V, with decreased binding observed in the presence of calcium (not shown). A greater degree of inhibition of Annexin V binding

to GST-β5 by the VISY peptide was observed in the presence of calcium (67% inhibition) than in the absence of calcium (45%) (FIG. 20A).

Penetratin peptide chimera binding to the β5 cytoplasmic domain induces programmed cell death.

The induction of apoptosis by VISY peptide was shown in Example 9 was confirmed. 10^6 HUVEC were treated with 15 μM of VISY antennapedia (penetratin) chimera or 15 μM of antennapedia peptide (pentratin) alone for 2-4 hours and chromatin fragmentation was analyzed by electrophoresis in an agarose gel. FIG. 21 shows the induction of apoptosis by VISY-Ant (penetratin), as indicated by chromatin fragmentation. Neither VISY or penetratin alone induced apoptosis. Induction of apoptosis was inhibited up to 70% when a caspase inhibitor (zVAD, caspase inhibitor I, Calbiochem #627610, San Diego, CA) was added to the media at the same time as the VISY chimeric peptide.

A distinction between the mechanism of cell death induced by VISY peptide and other pro-apoptosis agents is that other apoptotic mechanisms evaluated in cell culture typically involve detachment of the cells from the substrate, followed by cell death. In contrast, in VISY induced cell death, the cells do not detach from the substrate before dying. Thus, endothanos (death from inside) appears to differ from anoikis (homelessness).

Example 9 and the present results show that VISY peptides activate an integrin dependent apoptosis pathway. The present example shows that the endogenous analog for VISY peptide in Annexin V. These results demonstrate the existence of a novel apoptotic pathway, mediated through an interaction between Annexin V and β5 integrin and dependent on caspase activity. This novel apoptotic mechanism is termed endothanos. The skilled artisan will realize that the existence of a novel mechanism for inducing or inhibiting apoptosis is of use for a variety of applications, such as cancer therapy.

Example 8. Identification of Receptor/Ligand Pairs: Aminopeptidase A regulates endothelial cell function and angiogenesis

Endothelial cells in tumor vessels express specific angiogenic markers. Aminopeptidase A (APA, EC 3.4.11.7) is upregulated in microvessels undergoing angiogenesis. APA is a homodimeric, membrane-bound zinc metallopeptidase that hydrolyzes N-terminal glutamyl or aspartyl residues from oligopeptides (Nanus *et al.*, 1993). *In vivo*, APA converts angiotensin II to angiotensin III. The renin-angiotensin system plays an important role in regulating several endocrine, cardiovascular, and behavioral functions (Ardaillou, 1997; Stroth and Unger, 1999). Recent studies also suggest a role for angiotensins in angiogenesis (Andrade *et al.*, 1996), but the function of APA in the angiogenic process has not been investigated so far.

In the present example, targeting peptides capable of binding APA were identified by screening phage libraries on APA-expressing cells. APA-binding peptides containing the motif CPRECESIC (SEQ ID NO:123) specifically inhibited APA enzyme activity. Soluble CPRECESIC (SEQ ID NO:123) peptide inhibited migration, proliferation, and morphogenesis of endothelial cells *in vitro* and interfered with *in vivo* angiogenesis in a chick embryo chorioallantoic membrane (CAM) assay. Furthermore, APA null mice had a decreased amount of retinal neovascularization compared to wild type (wt) mice in hypoxia-induced retinopathy in premature mice. These results may lead to a better understanding of the role of APA in angiogenesis and to development of new anti-tumor therapeutic strategies.

Materials and Methods

Cell cultures

The renal carcinoma cell line SK-RC-49 was transfected with an expression vector encoding full-length APA cDNA (Geng *et al.*, 1998). Cells were maintained in MEM (Irvine Scientific, Santa Ana, CA), supplemented with 2 mM glutamine, 1% nonessential amino acids, 1% vitamins (Gibco BRL), 100 U/ml streptomycin, 100 U/ml penicillin (Irvine Scientific), 10 mM sodium pyruvate (Sigma-Aldrich), and 10% fetal

calf serum (FCS) (Tissue Culture Biological, Tulare, CA). Stably transfected cells were maintained in G418-containing medium. HUVECs were isolated by collagenase treatment and used between passages 1 to 4. Cells were grown on gelatin-coated plastic in M199 medium (Sigma) supplemented with 20% FCS, penicillin (100 U/ml), streptomycin (50 μg/ml), heparin (50 μg/ml), and bovine brain extract (100 μg/ml). All media supplements were obtained commercially (Life Technologies, Inc., Milan, Italy).

Antibodies and peptides

The anti-APA mAb RC38 (Schlingemann *et al.*, 1996) was used to immunocapture APA from transfected cell lysates. CPRECESIC (SEQ ID NO:123) and GACVRLSACGA (SEQ ID NO:124) cyclic peptides were chemically synthesized, spontaneously cyclized in non-reducing conditions, and purified by mass spectrometry (AnaSpec San Jose, CA). The mass spectrometer analysis of the CPRECESIC (SEQ ID NO:123) peptide revealed six different peaks, possibly reflecting different positions of disulfide bounds and the formation of dimers. Due to the similar biochemical behavior of the different fractions on APA enzyme activity, a mix of the six peaks was used in all procedures described below.

APA immunocapture

Cells were scraped from semi-confluent plates in cold PBS containing 100 mM N-octyl-β-glucopyranoside (Calbiochem), lysed on ice for 2 h, and centrifuged at 13,000 x *g* for 15 min. Microtiter round-bottom wells (Falcon) were coated with 2 μg of RC38 for 4 h at room temperature and blocked with PBS/3% BSA (Intergen, Purchase, NY) for 1 h at room temperature, after which 150 μl of cell lysate (1 mg/ml) was incubated on the mAb-coated wells overnight at 4°C, washed five times with PBS/0.1% Tween-20 (Sigma), and washed twice with PBS.

APA enzyme assay

Cells and immunocaptured proteins were tested for specific enzyme activity according to Liln *et al.* (1998). Briefly, adherent cells or RC38-immunocaptured cell

extracts were incubated for 2 h at 37°C with PBS containing 3 mM α-L-glutamyl-p-nitroanilide (Fluka) and 1 mM $CaCl_2$. Enzyme activity was determined by reading the optical absorbance (O.D.) at 405 nm in a microplate reader (Molecular Devices, Sunnyvale, CA).

Cell panning

A $CX_3CX_3CX_3C$ (C, cysteine; X, any amino acid) library was prepared (Rajotte *et al.*, 1998). Amplification and purification of phage particles and DNA sequencing of phage-displayed inserts were performed as described above. Cells were detached by incubation with 2.5 mM EDTA in PBS, washed once in binding medium (DMEM high glucose supplemented with 20 mM HEPES and 2% FCS), and resuspended in the same medium at a concentration of $2x10^6$ cells/ml. 10^{10} TU of phage were added to 500 µl of the cell suspension, and the mixture was incubated overnight (first round) or for 2 h (successive rounds) at 4°C with gentle rotation. Cells were washed five times in binding medium at room temperature and resuspended in 100 µl of the same medium. Phage were rescued by adding 1 ml of exponentially growing K91Kan *Escherichia coli* bacteria and incubating the mixture for 1 h at room temperature. Bacteria were diluted in 10 ml of LB medium supplemented with 0.2 µg/ml tetracycline and incubated for another 20 min at room temperature. Serial dilutions were plated on LB plates containing 40 µg/ml tetracycline, and plates were incubated at 37°C overnight before colonies were counted.

Phage binding specificity assay

The cell binding assay was performed with an input of 10^9 TU as described for the cell panning. The specificity was confirmed by adding CPRECESIC (SEQ ID NO:123) peptide to the binding medium in increasing concentrations. For phage binding on immunocaptured APA, wells were blocked for 1 h at room temperature with PBS/3% BSA and incubated with 10^9 TU for 1 h at room temperature in 50 µl PBS/3% BSA. After eight washes in PBS/1% BSA/0.01% Tween-20 and two washes in PBS,

phage were rescued by adding 200 µl of exponentially growing K91Kan *E. coli*. Each experiment was repeated at least three times.

In vivo tumor homing of APA-binding phage

MDA-MB-435-derived tumor xenografts were established in female nude mice 2 months old (Jackson Labs, Bar Harbor, Maine). Mice were anesthetized with Avertin and injected intravenously through the tail vein with 10^9 TU of the phage in a 200 µl volume of DMEM. The phage were allowed to circulate for 5 min, and the animals were perfused through the heart with 5 ml of DMEM. The tumor and brain were dissected from each mouse, weighed, and equal amounts of tissue were homogenized. The tissue homogenates were washed three times with ice-cold DMEM containing a proteinase inhibitor cocktail and 0.1% BSA. Bound phage were rescued and counted as described for cell panning. Fd-tet phage was injected at the same input as a control. The experiment was repeated twice. In parallel, part of the same tissue samples were fixed in Bouin solution, and imbedded in paraffin for preparation of tissue sections. An antibody to M-13 phage (Amersham-Pharmacia) was used for the staining.

Cell growth assay

HUVECs were seeded in 48-well plates (10^4 cells/well) and allowed to attach for 24 h in complete M199 medium. The cells were then starved in M199 medium containing 2% FCS for 24 h. CPRECESIC (SEQ ID NO:123) or control GACVRLSACGA (SEQ ID NO:124) peptide (1 mM) was added to the wells in medium containing 2% FCS and 10 ng/ml VEGF-A (R&D System, Abingdom, UK). After incubation for the indicated times, cells were fixed in 2.5% glutaraldehyde, stained with 0.1% crystal violet in 20% methanol, and solubilized in 10% acetic acid. All treatments were done in triplicate. Cell growth was evaluated by measuring the O.D. at 590 nm in a microplate reader (Biorad, Hercules, CA). A calibration curve was established and a linear correlation between O.D. and cell counts was observed between 10^3 and 10^5 cells.

Chemotaxis assay

A cell migration assay was performed in a 48-well microchemotaxis chamber (NeuroProbe, Gaithersburg, MD) according to Bussolini *et al.* (1995). Polyvinylpyrrolidone-free polycarbonate filters (Nucleopore, Cambridge, MA) with 8-μm pores were coated with 1% gelatin for 10 min at room temperature and equilibrated in M199 medium supplemented with 2% FCS. CPRECESIC (SEQ ID NO:123) or control GACVRLSACGA (SEQ ID NO:124) peptide (1 mM) was placed in the lower compartment of a Boyden chamber in M199 medium supplemented with 2% FCS and 10 ng/ml VEGF-A (R&D System). Subconfluent cultures that had been starved overnight were harvested in PBS containing 2.5 mM EDTA, washed once in PBS, and resuspended in M199 medium containing 2% FCS at a final concentration of 2×10^6 cells/ml. After the filter was placed between the lower and upper chambers, 50 μl of the cell suspension was seeded in the upper compartment, and cells were allowed to migrate for 5 h at 37°C in a humidified atmosphere with 5% CO_2. The filter was then removed, and cells on the upper side were scraped with a rubber policeman. Migrated cells were fixed in methanol and stained with Giemsa solution (Diff-Quick, Baxter Diagnostics, Rome, Italy). Five random high-power fields (magnitude 100×) were counted in each well. Each assay was run in triplicate.

Three-dimensional cell culture

Matrigel (Collaborative Research, Bedford, MA) was added at 100 μl per well to 48-well tissue culture plates and allowed to solidify for 10 min at 37°C. HUVECs were starved for 24 h in M199 medium supplemented with 2% FCS before being harvested in PBS containing 2.5 mM EDTA. 10^4 cells were gently added to each of the triplicate wells and allowed to adhere to the gel coating for 30 min at 37°C. Then, medium was replaced with indicated concentrations of CPRECESIC (SEQ ID NO:123) or GACVRLSACGA (SEQ ID NO:124) peptides in complete medium. The plates were

photographed after 24 h with an inverted microscope (Canon). The assay was repeated three times.

CAM assay

In vivo angiogenesis was evaluated by a CAM assay (Ribatti *et al.*, 1994). Fertilized eggs from White Leghorn chickens were maintained in constant humidity at 37°C. On the third day of incubation, a square window was opened in the eggshell and 2–3 ml of albumen was removed to detach the developing CAM from the shell. The window was sealed with a glass plate of the same size and the eggs were returned to the incubator. At day 8, 1 mm^3 sterilized gelatin sponges (Gelfoam, Upjohn Co, Kalamazoo, Milan) were adsorbed with VEGF-A (20 ng, R&D System) and either CPRECESIC (SEQ ID NO:123) or control GACVRLSACGA (SEQ ID NO:124) peptide (1 mM) in 3 µl PBS and implanted on the top of the growing CAMs under sterile conditions. CAMs were examined daily until day 12 and photographed *in ovo* with a Leica stereomicroscope. Capillaries emerging from the sponge were counted. The assay was repeated twice.

Induction of retinal neovascularization

APA null mice have been described (Lin *et al.*, 1998). Mice pups on P7 (7^{th} day post-partum) with their nursing mothers were exposed to 75% oxygen for 5 days. Mice were brought back to normal oxygen (room air) on P12. For histological analysis mice were killed between P17 and P21 and eyes were enucleated and fixed in 4% paraformaldehyde in PBS overnight at +4°C. Fixed eyes were imbedded in paraffin and 5 µm serial sections were cut. Sections were stained with hematoxylin/eosin (h/e) solution. Neovascular nuclei on the vitreous side of the internal limiting membrane were counted from 20 h/e–stained sections per each eye. The average number of neovascular nuclei per section was calculated and compared between animal groups using Student's t-test.

Results

Cell panning with phage display select an APA-binding motif

To identify a peptide capable of binding to APA, cells were screened with a random peptide phage library. First, SK-RC-49 renal carcinoma cells, which do not express APA, were transfected with full-length APA cDNA to obtain a model of APA expression in the native conformation. APA expressed as a result of transfection was functionally active, as evidenced by an APA enzyme assay (not shown), but parental SK-RC-49 cells showed neither APA expression nor activity (not shown).

The $CX_3CX_3CX_3C$ phage library (10^{10} transducing units [TU]) was preadsorbed on parental SK-RC-49 cells to decrease nonspecific binding. Resuspended SK-RC-49/APA cells were screened with phage that did not bind to the parent cells. SK-RC-49/APA-bound phage were amplified and used for two consecutive rounds of selection. An increase in phage binding to SK-RC-49/APA cells relative to phage binding to SK-RC-49 parental cells was observed in the second and third rounds (not shown).

Subsequent sequencing of the phage revealed a specific enrichment of a peptide insert, CYNLCIRECESICGADGACWTWCADGCSRSC (SEQ ID NO:125), with a tandem repetition of the general library sequence $CX_3CX_3CX_3C$. This sequence represented 50% of 18 randomly selected phage inserts from round 2 and 100% of phage inserts from round 3. Four peptide inserts derived from round 2 shared sequence similarity with the tandem phage (Table 12, in bold font). Several other apparently conserved motifs were observed among round 2 peptides (Table 12, underlined or italicized). One of these overlapped in part with the tandem repeated sequence. A search for sequence homology of the selected peptides against human databases did not yield a significant match.

Table 12. APA-binding peptide sequences.

Peptide sequences [a]	Round 2 (%)	Round 3 (%)
CYNLCI**RECESIC**GADGACWTWCADGCSRSC (SEQ ID NO:125)	50	100
CLGQCA**SIC**VNDC (SEQ ID NO:126)	5	-
CPKVCP**RECES**NC (SEQ ID NO:127)	5	-
CGTGCAVECEVVC (SEQ ID NO:128)	5	-
CAVACWADCQLGC (SEQ ID NO:129)	5	-
CSGLCTVQ*CLEGC* (SEQ ID NO:130)	5	-
CSMM*CLEGC*DDWC (SEQ ID NO:131)	5	-
OTHER	20	-

Selected phage inserts are specific APA ligands.

Phage displaying the peptide inserts CYNLCI**RECESIC**GADGACWTWCADGCSRSC (SEQ ID NO:125), CPKV**CPRECES**NC (SEQ ID NO:127) or CLGQCA**SIC**VNDC (SEQ ID NO:126) were individually tested for APA binding. All three phage specifically bound to the

surface of SK-RC-49/APA cells (not shown), with a similar pattern of 6-fold enrichment relative to SK-RC-49 parental cells. Control, insertless phage showed no binding preference (not shown). CGTGCAV**ECE**VVC (SEQ ID NO:128) and the other phage selected in round 2 showed no selective binding to SK-RC-49/APA cells (data not shown). A soluble peptide, CPRECESIC (SEQ ID NO:123) containing a consensus sequence reproducing the APA-binding phage inserts was synthesized.

Binding assays were performed with CPKV**CPRECES**NC (SEQ ID NO:127) phage in the presence of the CPRECESIC (SEQ ID NO:123) peptide. Soluble CPRECESIC (SEQ ID NO:123) peptide competed with CPKV**CPRECES**NC (SEQ ID NO:127) phage for binding to SK-RC-49/APA cells, but had no effect on nonspecific binding to SK-RC-49 parental cells (not shown. The unrelated cyclic peptide GACVRLSACGA (SEQ ID NO:124) had no competitive activity (not shown). Binding of CYNL**CIRECESIC**GADGACWTWCADGCSRSC (SEQ ID NO:125) phage was also displaced by CPRECESIC (SEQ ID NO:123) peptide, but the binding of CLGQCA**SIC**VNDC (SEQ ID NO:126) phage was not affected (data not shown).

To further confirm the substrate specificity of the selected peptide inserts, APA was partially purified from APA-transfected cell extracts by immunocapture with mAb RC38. The APA protein immobilized on RC38-coated microwells was functional, as confirmed by enzyme assay (not shown). The CYNL**CIRECESIC**GADGACWTWCADGCSRSC (SEQ ID NO:125), CPKV**CPRECES**NC (SEQ ID NO:127), and CLGQCA**SIC**VNDC (SEQ ID NO:126) phage selectively bound immunocaptured APA, with a 10- to 12-fold enrichment compared to phage binding to RC38-immunocaptured cell lysates from SK-RC-49 parental cells (not shown).

APA-binding phage target tumors in vivo.

The ability of the identified peptide to home to tumors was evaluated, using nude mice implanted with human breast tumor xenografts as a model system. Phage were injected into the tail vein of tumor-bearing mice, and targeting was evaluated by

phage recovery from tissue homogenates. CPKVCPRECESNC (SEQ ID NO:127) phage was enriched 4-fold in tumor xenografts compared to brain tissue, which was used as a control (FIG. 22). Insertless phage did not target the tumors (FIG. 22). Neither CYNLCIRECESICGADGACWTWCADGCSRSC (SEQ ID NO:125) nor CLGQCASICVNDC (SEQ ID NO:126) phage showed any tumor-homing preference (data not shown).

The homing of CPKVCPRECESNC (SEQ ID NO:127) was confirmed by anti-M13 immunostaining on tissue sections (not shown). Strong phage staining was apparent in tumor vasculature but not in normal vasculature (not shown). Insertless phage did not bind to tumor vessels.

CPRECESIC (SEQ ID NO:123) is a specific inhibitor of APA activity.

To investigate the effect of CPRECESIC (SEQ ID NO:123) on APA enzyme activity, SK-RC-49/APA cells were incubated with the APA specific substrate α-glutamyl-p-nitroanilide in the presence of increasing concentrations of either CPRECESIC (SEQ ID NO:123) or control GACVRLSACGA (SEQ ID NO:124) peptides. Enzyme activity was evaluated by a colorimetric assay after 2 h incubation at 37°C. CPRECESIC (SEQ ID NO:123) inhibited APA enzyme activity, reducing the activity by 60% at the highest concentration tested (FIG. 23). The IC_{50} of CPRECESIC (SEQ ID NO:123) for enzyme inhibition was calculated to be 800 μM. CPRECESIC (SEQ ID NO:123) did not affect the activity of a closely related protease, aminopeptidase N (data not shown).

CPRECESIC (SEQ ID NO:123) inhibits migration and proliferation of endothelial cells.

The potential use of CPRECESIC (SEQ ID NO:123) peptide as an anti-angiogenic drug was determined. First, the effect of APA inhibition by CPRECESIC (SEQ ID NO:123) peptide *in vitro* on the migration and proliferation of human umbilical vein endothelial cells (HUVECs) stimulated with VEGF-A (10 ng/ml) was examined. The presence of functional APA on HUVECs was evaluated by enzyme

assay (not shown). At the highest concentration tested (1 mM), CPRECESIC (SEQ ID NO:123) peptide inhibited chemotaxis of HUVECs by 70% in a Boyden chamber assay (FIG. 24). At the same peptide concentration, cell proliferation was inhibited by 50% (FIG. 25). Lower concentrations of CPRECESIC (SEQ ID NO:123) peptide or the GACVRLSACGA (SEQ ID NO:124) control peptide had no significant effect on cell migration or proliferation (not shown).

CPRECESIC (SEQ ID NO:123) inhibits angiogenesis in vitro and in vivo

The inhibitory effect of CPRECESIC (SEQ ID NO:123) peptide in different *in vitro* and *in vivo* models of angiogenesis was examined. HUVECs plated on a three-dimensional matrix gel differentiate into a capillary-like structure, providing an *in vitro* model for angiogenesis. Increasing concentrations of CPRECESIC (SEQ ID NO:123) peptide resulted in a progressive impairment of the formation of this network (not shown). At a peptide concentration of 1 mM, vessel-like branching structures were significantly fewer and shorter, and as a result, the cells could not form a complete network organization (not shown). The control peptide GACVRLSACGA (SEQ ID NO:124) did not affect HUVEC morphogenesis (not shown).

A commonly used model of simplified *in vivo* angiogenesis is the chicken chorioallantoic membrane (CAM), in which neovascularization can be stimulated during embryonic development. An appropriate stimulus, adsorbed on a gelatin sponge, induces microvessel recruitment to the sponge itself, accompanied by remodeling and ramification of the new capillaries. Eight-day-old chicken egg CAMs were stimulated with VEGF-A alone (20 ng) or with VEGF-A plus CPRECESIC (SEQ ID NO:123) or GACVRLSACGA (SEQ ID NO:124) (1 mM) peptides. The CAMs were photographed at day 12. Neovascularization induced by VEGF-A was inhibited by CPRECESIC (SEQ ID NO:123) by 40% based on the number of capillaries emerging from the sponge (Table 13). The neovessels did not show the highly branching capillary structures typically seen after VEGF-A stimulation (not shown). Treatment with control peptide GACVRLSACGA (SEQ ID NO:124) or with lower

peptide concentrations of CPRECESIC (SEQ ID NO:123) had no effect on the number of growing vessels (not shown).

Table 13. CAM assay for angiogenesis

TREATMENT	BLOOD VESSEL NUMBERS
No VEGF-A	12.0 ± 2.82*
VEGF-A	57.0 ± 1.41*
VEGF-A + control	56.5 ± 2.12
VEGF-A + CPRECESIC (SEQ ID NO:123)	5.5 ± 1.41*

*p< 0.01 with the Student-Newman-Keuls test. The results are expressed as the mean and standard error from two independent experiments.

APA-deficient mice show impaired neovascularization

The ability of $APA^{+/-}$ and $APA^{-/-}$ null mice to undergo neovascularization was examined in a model of hypoxic retinopathy in premature mice. Induction of retinal neovascularization by relative hypoxia was already present in $APA^{+/-}$ mice compared to wild type mice (not shown). Neovascularization was almost undetectable in APA null mice (not shown). Neovascularization was quantified by counting vitreous protruding neovascular nuclei from 20 sections of hypoxic eyes. Significant induction of retinal neovascularization (16.17 ± 1.19 neovascular nuclei/eye section) was seen in the wild type mice on postnatal day 17 (P17) after 75% oxygen treatment from P7 to P12. Decreased amounts of neovascular nuclei were seen in the retinas of $APA^{+/-}$ (10.76 ± 1.03 neovascular nuclei/eye section) and APA null (4.25 ± 0.45 neovascular nuclei/eye section) mice on P17 after exposure to 75% oxygen from P7 to P12.

Discussion

In vivo, APA is overexpressed by activated microvessels, including those in tumors, but it is barely detectable in quiescent vasculature, making it a suitable target for vessel-directed tumor therapy. The present example identified a novel targeting peptide ligand for APA, CPRECESIC (SEQ ID NO:123). Soluble CPRECESIC (SEQ ID NO:123) peptide inhibited APA enzyme activity with an IC_{50} of 800 μM.

Using cultured HUVECs as an *in vitro* model of angiogenesis, soluble CPRECESIC (SEQ ID NO:123) peptide inhibited VEGF-A-induced migration and proliferation of HUVECs. These data are consistent with a requirement for migration and proliferation of endothelial cells during angiogenesis. CPRECESIC (SEQ ID NO:123) also blocked the formation of capillary-like structures in a Matrigel model and inhibited angiogenesis in VEGF-A-stimulated CAMs.

APA was shown to be important player in neovascularization induced by relative hypoxia, since APA null mice had significatively less retinal neovascularization compared to wt mice. These results strengthen the potential of using APA as a specific target for the inhibition of tumor angiogenesis.

In summary, the soluble peptide CPRECESIC (SEQ ID NO:123) is a selective APA ligand and inhibitor. The inhibition of APA by CPRECESIC (SEQ ID NO:123) led to the inhibition of angiogenesis in different *in vitro* and *in vivo* assays, demonstrating for the first time a prominent role for APA in the angiogenic process. Furthermore, APA-binding phage can home to tumor blood vessels, suggesting possible therapeutic uses of CPRECESIC (SEQ ID NO:123) as an inhibitor of tumor neovascularization. The endogenous analog of CPRECESIC (SEQ ID NO:123) may be identified by antibody based purification or identification methods, similar to those disclosed above.

Example 9. Screening Phage Libraries by PALM

In certain embodiments, it is desirable to be able to select specific cell types from a heterogeneous sample of an organ or tissue. One method to accomplish such selective sampling is by PALM (Positioning and Ablation with Laser Microbeams).

The PALM Robot-MicroBeam uses a precise, computer-guided laser for microablation. A pulsed ultra-violet (UV) laser is interfaced into a microscope and focused through an objective to a beam spot size of less than 1 micrometer in diameter. The principle of laser cutting is a locally restricted ablative photodecomposition process without heating (Hendrix, 1999). The effective laser energy is concentrated on the minute focal spot only and most biological objects are transparent for the applied laser wavelength. This system appears to be the tool of choice for recovery of homogeneous cell populations or even single cells or subcellular structures for subsequent phage recovery. Tissue samples may be retrieved by circumcising a selected zone or a single cell after phage administration to the subject. A clear-cut gap between selected and non-selected area is typically obtained. The isolated tissue specimen can be ejected from the object plane and catapulted directly into the cap of a common microfuge tube in an entirely non-contact manner. The basics of this so called Laser Pressure Catapulting (LPC) method is believed to be the laser pressure force that develops under the specimen, caused by the extremely high photon density of the precisely focused laser microbeam. This tissue harvesting technique allows the phage to survive the microdissection procedure and be rescued.

PALM was used in the present example to select targeting phage for mouse pancreatic tissue, as described below.

Materials and Methods

In vivo and in situ Panning

A CX_7C peptide phage library (10^9 TU) was injected into the tail vein of a C57BL/6 male mouse, and the pancreas was harvested to recover the phage by bacterial infection. Phage from 246 colonies were grown separately in 5 mls LB/kanamycin (100 μg/ml)/tetracycline (40 μg/ml) at 37°C in the dark with agitation. Overnight cultures

were pooled and the phage purified by NaCl/PEG precipitation for another round of *in vivo* bio-panning. Three hundred colonies were picked from the second round of panning, and the phage were recovered by precipitation. Phage from the second bio-panning round was then used for another round of *in vivo* panning and also was incubated with thawed frozen murine pancreatic sections for one *in situ* panning round.

For the third *in vivo* panning round, 10^9 TU phage from the second round were injected into a third mouse and allowed to circulate for six minutes, followed by an intravenous injection of 50 µl of FITC-lectin (Vector Laboratories, Inc.). After a two-minute circulation, the mouse was perfused through the left ventricle with 3 mls MEM Earle salts. The pancreas was harvested, frozen at -80 °C in Tissue Tek (Sakura), and sectioned onto prepared slides.

For the third *in situ* round, purified phage, isolated from the second round, were incubated with 4-14 µm thawed murine pancreatic sections on ice for 30 minutes. Sections were rinsed with 100 µl ice-cold PBS 8x at room temperature (RT). Bound phage were recovered from each section by adding 100 µl K91 Kan^R (OD_{600} = 2.03) to infect at RT for 30-60 minutes. Infected K91 KanR were withdrawn from each section and allowed to recover in 10 mls LB/Kan/Tet (0.2 µg/ml) for 20 minutes in the dark. Aliquots from the each culture were plated out onto LB/Kan/Tet (40 µg/ml) plates and incubated overnight in the dark at 37 °C. The tetracycline concentration of the remainder of each culture was increased to 40 µg/ml and the cultures were incubated overnight at 37 °C in the dark with agitation for phage amplification and purification.

DNA Amplification

Phage were recovered from cryo-preserved FITC-lectin stained mouse pancreatic islets and surrounding acinar cells that were microdissected from 14 µm sections using the PALM (Positioning and Ablation with Laser Microbeams) cold laser pressure catapulting system. Pancreatic islet and control sections were catapulted into 1 mM EDTA, pH 8, and frozen at -20 °C until enough material was collected for PCR amplification. Phage DNA was amplified with fUSE5 primers: forward primer 5' TAA

TAC GAC TCA CTA TAG GGC AAG CTG ATA AAC CGA TAC AATT 3' (SEQ ID NO:132), reverse primer 5' CCC TCA TAG TTA GCG TAA CGA TCT 3' (SEQ ID NO:133). The PCR products were subjected to another round of PCR using a nested set of primers. The 3' end of the second primer set was tailed with the M13 reverse primer for sequencing purposes. The nested primer set used was: forward nested primer 5' CCTTTCTATTCTCACTCGGCCG 3' (SEQ ID NO:134), reverse nested primer 5' CAGGAAACAGCTATGACCGCTAAACAACTTTCAACAGTTTCGGC 3' (SEQ ID NO:135). To generate peptide insert sequence containing flanking SfiI restriction sites, two more primers were used: forward library primer 5' CACTCGGCCGACGGGGC 3' (SEQ ID NO:136), reverse primer 5' CAGTTTCGGCCCCAGCGGCCC 3' (SEQ ID NO:137). PCR products generated from the nested primers were gel purified (Qiagen), and confirmed for the presence of a CX_7C peptide insert sequence using the M13 reverse primer by automated sequencing. PCR products generated from the library primers were gel purified (Qiagen), ligated into $CsCl_2$ purified fUSE5/SfiI, electroporated into electrocompetent MC1061 cells, and plated onto LB/streptomycin (100 μg/ml)/tetracycline (40 μg/ml) agar plates. Single colonies were subjected to colony PCR using the fUSE5 primers to verify the presence of a CX_7C insert sequence by gel electrophoresis. Positive clones were sequenced using BigDye terminators (Perkin Elmer)

Phage Infection

Pancreatic islet and control sections were catapulted into 1 mM AEBSF, 20 μg/ml aprotinin, 10 μg/ml leupeptin, 1 mM elastase inhibitor I, 0.1 mM TPCK, 1 nM pepstatin A in PBS, pH 7.4, and frozen for 48 hours or less until enough material was collected. The sections were thawed on ice and the volume adjusted to 200 μl with PBS, pH 7.4. Samples were incubated with 1 ml K91 Kan^R (OD = 0.22) for two hours at RT on a nutator. Each culture was transferred to 1.2 mls LB/Kan/Tet (0.2 μg/ml) and incubated in the dark at RT for 40 minutes. The tetracycline concentration was increased to 40 μg/ml for each culture, and the cultures were incubated overnight at 37

°C with agitation. Each culture was plated out the following day onto LB/Kan/Tet agar plates and incubated for 14 hours at 37 °C in the dark. Positive clones were picked for colony PCR and automated sequencing.

Results

The general schem for *in vivo* panning using PALM is illustrated in FIG. 26. After an initial round of *in vivo* selection, phage were either bulk amplified or else single colonies of phage from pancreas, kidney, lung and adrenal glands were amplified and subjected to additional rounds of *in vivo* screening. Both bulk amplified and colony amplified phage from mouse pancreas showed successive enrichment with increasing rounds of selection (not shown). After three rounds of selection, the colony amplified phage showed almost an order of magnitude higher enrichment than bulk amplified phage (not shown).

Table 14 lists selected targeting sequences and consensus motifs identified by pancreatic screening.

Table 14. Pancreatic targeting peptides and motifs

Motif	Peptide Sequence
GGL	CVPGLGGLC (SEQ ID NO:139)
(SEQ ID NO:138)	CGGLDVRMC (SEQ ID NO:140)
	CDGGLDWVC (SEQ ID NO:141)
LGG	CVPGLGGLC (SEQ ID NO:139))
(SEQ ID NO:142)	CTWLGGREC (SEQ ID NO:143)
	CSRWGLGGC (SEQ ID NO:144)
	CPPLGGSRC (SEQ ID NO:251)
VRG	CVGGVRGGC (SEQ ID NO:146)
(SEQ ID NO:145)	CVGNDVRGC (SEQ ID NO:147)
	CESRLVRGC (SEQ ID NO:148)
	CGGRPVRGC (SEQ ID NO:149)
AGG	CTPFIAGGC (SEQ ID NO:151)

(SEQ ID NO:150)	CREWMAGGC (SEQ ID NO:152)
	CAGGSLRVC (SEQ ID NO:153)
VVG	CEGVVGIVC (SEQ ID NO:155)
(SEQ ID NO:154)	CDSVVGAWC (SEQ ID NO:156)
	CRTAVVGSC (SEQ ID NO:157)
VGG	CVGGARALC (SEQ ID NO:159)
(SEQ ID NO:158)	CVGGVRGGC (SEQ ID NO:147)
	CLAHRVGGC (SEQ ID NO:160)
GGL	CWALSGGLC (SEQ ID NO:162)
(SEQ ID NO:161)	CGGLVAYGC (SEQ ID NO:163)
	CGGLATTTC (SEQ ID NO:164)
GRV	CGRVNSVAC (SEQ ID NO:166)
(SEQ ID NO:165)	CAGRVALRC (SEQ ID NO:167)
GGA	CWNGGARAC (SEQ ID NO:169)
(SEQ ID NO:168)	CLDRGGAHC (SEQ ID NO:170)
GVV	CELRGVVVC (SEQ ID NO:172)
(SEQ ID NO:171)	
GGV	CIGGVHYAC (SEQ ID NO:174)
(SEQ ID NO:173)	CGGVHALRC (SEQ ID NO:175)
GMWG	CIREGMWGC (SEQ ID NO:177)
(SEQ ID NO:176)	CIRKGMWGC (SEQ ID NO:178)
ALR	CGGVHALRC (SEQ ID NO:175)
(SEQ ID NO:179)	CAGRVALRC (SEQ ID NO:167)
	CEALRLRAC (SEQ ID NO:180)

ALV	CALVNVHLC (SEQ ID NO:182)
(SEQ ID NO:181)	CALVMVGAC (SEQ ID NO:183)
GGVH	CGGVHALRC (SEQ ID NO:175)
(SEQ ID NO:184)	CIGGVHYAC (SEQ ID NO:174)
VSG	CMVSGVLLC (SEQ ID NO:186)
(SEQ ID NO:185)	CGLVSGPWC (SEQ ID NO:187)
	CLYDVSGGC (SEQ ID NO:188)
GPW	CSKVGPWWC (SEQ ID NO:190)
(SEQ ID NO:189)	CGLVSGPWC (SEQ ID NO:191)
none	CAHHALMEC (SEQ ID NO:192)
	CERPPFLDC (SEQ ID NO:193)

FIG. 27 shows a general protocol for recovery of phage insert sequences from PALM selected thin section materials. As indicated, phage may be recovered by direct infection of *E. coli* host bacteria, after protease digestion of the thin section sample. Alternatively, phage inserts may be recovered by PCR amplification and cloned into new vector DNA, then electroporated or otherwise transformed into host bacteria for cloning.

Both methods of PALM recovery of phage were successful in retrieving pancreatic targeting sequences. Pancreatic sequences recovered by direct bacterial infection included CVPRRWDVC (SEQ ID NO:194), CQHTSGRGC (SEQ ID NO:195), CRARGWLLC (SEQ ID NO:196), CVSNPRWKC (SEQ ID NO:197), CGGVHALRC (SEQ ID NO:175), CFNRTWIGC (SEQ ID NO:198) and CSRGPAWGC (SEQ ID NO:199). Pancreatic targeting sequences recovered by amplification of phage inserts and cloning into phage include CWSRGQGGC (SEQ ID NO:200), CHVLWSTRC (SEQ ID NO:201), CLGLLMAGC (SEQ ID NO:202), CMSSPGVAC (SEQ ID NO:203), CLASGMDAC (SEQ ID NO:204), CHDERTGRC

(SEQ ID NO:205), CAHHALMEC (SEQ ID NO:206), CMQGAATSC (SEQ ID NO:207), CMQGARTSC (SEQ ID NO:208) and CVRDLLTGC (SEQ ID NO:209).

FIG. 28 through FIG. 31 show sequence homologies identified for selected pancreatic targeting sequences. Several proteins known to be present in pancreatic tissues are identified. The results of this example show that the PALM method may be used for selecting cell types from tissue thin sections and recovering targeting phage sequences. The skilled artisan will realize that this method could be used with virtually any tissue to obtain targeting sequences directed to specific types of cells in heterologous organs or tissues.

* * *

All of the COMPOSITIONS, METHODS and APPARATUS disclosed and claimed herein can be made and executed without undue experimentation in light of the presentdisclosure. While the compositions and methods of this invention have been described interms of preferred embodiments, it are apparent to those of skill in the art that variations maybe applied to the COMPOSITIONS, METHODS and APPARATUS and in the steps or in the sequence of steps of the methods described herein without departing from the concept, spirit and scope of the invention. More specifically, it are apparent that certain agents that are both chemically and physiologically related may be substituted for the agents described herein while the same or similar results would be achieved. All such similar substitutes and modifications apparent to those skilled in the art are deemed to be within the spirit, scope and concept of the invention as defined by the appended claims.

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WHAT IS CLAIMED IS:

1. A method comprising

   a) injecting a subject with a phage display library;

   b) obtaining samples of one or more organs or tissues;

   c) producing thin sections of the samples; and

   d) recovering phage from the thin sections.

2. The method of claim 1, further comprising selecting one or more portions of a thin section by PALM (Positioning and Ablation with Laser Microbeams).

3. The method of claim 2, wherein the selected portion contains a specific cell type.

4. The method of claim 2, wherein the selected portion contains a homogenous population of cells.

5. The method of claim 3, wherein the cells are cancer cells.

6. The method of claim 1, wherein the phage are recovered by infecting bacteria with the phage.

7. The method of claim 1, wherein the phage are recovered by amplifying phage inserts and ligating the amplified inserts to phage DNA to produce new phage.

8. A method of preparing a phage display library comprising:

   a) immunizing a host animal with a target organ, tissue or cell type;

   b) obtaining mRNAs encoding antibodies from the host animal;

   c) preparing cDNAs from the mRNAs encoding antibodies; and

   d) preparing a phage display library from the cDNAs.

9. The method of claim 8, further comprising using antibody specific primers to amplify cDNAs that encode antibodies.

10. The method of claim 8, wherein the target organ, tissue or cell is diseased.

11. The method of claim 10, wherein the target comprises cancer cells.

12. The method of claim 8, further comprising: (i) injecting the phage display library into a subject; and (ii) recovering phage from one or more organs, tissues or cell types.

13. The method of claim 8, further comprising screening said library against a target protein or peptide.

14. A phage display library prepared by the method of claim 8.

15. A method of interfering with pregnancy comprising;

    a) obtaining a peptide comprising at least three contiguous amino acids of a sequence selected from SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44 or SEQ ID NO:45; and

    b) administering the peptide to a female subject.

16. The method of claim 15, wherein the subject is pregnant.

17. The method of claim 15, further comprising attaching an agent to the peptide.

18. A method of delivering an agent to a fetus comprising:

    a) obtaining a peptide comprising at least three contiguous amino acids of a sequence selected from SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44 or SEQ ID NO:45;

    b) attaching the peptide to an agent; and

    b) administering the peptide to a pregnant subject.

19. The method of claims 17 or 18, wherein the agent is a drug, a pro-apoptotic agent, an anti-angiogenic agent, an enzyme, a hormone, a cytokine, a growth factor, a cytotoxic agent, a peptide, a protein, an antibiotic, an antibody, a Fab fragment of an antibody, an imaging agent, an antigen, a survival factor, an anti-apoptotic agent, a hormone antagonist, a virus, a bacteriophage, a bacterium, a liposome, a microparticle, a microdevice, a cell or an expression vector.

20. A method of targeting delivery to adipose tissue comprising:
    a) obtaining a targeting peptide comprising an amino acid sequence of at least three contiguous amino acids selected from SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54 or SEQ ID NO:55;
    b) attaching the peptide to an agent to form a complex; and
    c) administering the complex to a subject.

21. The method of claim 20, further comprising inducing weight loss in said subject.

22. An isolated peptide of 100 amino acids or less in size, comprising at least 3 contiguous amino acids of a sequence selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:250.

23. The isolated peptide of claim 22, wherein said peptide is 50 amino acids or less in size.

24. The isolated peptide of claim 22, wherein said peptide is 25 amino acids or less in size.

25. The isolated peptide of claim 22, wherein said peptide is 10 amino acids or less in size.

26. The isolated peptide of claim 22, wherein said peptide is 7 amino acids or less in size.

27. The isolated peptide of claim 22, wherein said peptide is 5 amino acids or less in size.

28. The isolated peptide of claim 22, wherein said peptide comprises at least 5 contiguous amino acids of a sequence selected from any of SEQ ID NO:5

through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:250.

29. The isolated peptide of claim 22, wherein said peptide is attached to a molecule.

30. The isolated peptide of claim 29, wherein said molecule is a drug, a chemotherapeutic agent, a radioisotope, a pro-apoptosis agent, an anti-angiogenic agent, a hormone, a cytokine, a growth factor, a cytotoxic agent, a peptide, a protein, an antibiotic, an antibody, a Fab fragment of an antibody, an imaging agent, survival factor, an anti-apoptotic agent, a hormone antagonist or an antigen.

31. The isolated peptide of claim 30, wherein said pro-aptoptosis agent is selected from the group consisting of gramicidin, magainin, mellitin, defensin, cecropin, $(KLAKLAK)_2$ (SEQ ID NO:1), $(KLAKKLA)_2$ (SEQ ID NO:2), $(KAAKKAA)_2$ (SEQ ID NO:3) and $(KLGKKLG)_3$ (SEQ ID NO:4).

32. The isolated peptide of claim 30, wherein said anti-angiogenic agent is selected from the group consisting of thrombospondin, angiostatin5, pigment epithelium-drived factor, angiotensin, laminin peptides, fibronectin peptides, plasminogen activator inhibitors, tissue metalloproteinase inhibitors, interferons, interleukin 12, platelet factor 4, IP-10, Gro-ß, thrombospondin, 2-methoxyoestradiol, proliferin-related protein, carboxiamidotriazole, CM101, Marimastat, pentosan polysulphate, angiopoietin 2 (Regeneron), interferon-alpha, herbimycin A, PNU145156E, 16K prolactin fragment, Linomide, thalidomide, pentoxifylline, genistein, TNP-470, endostatin, paclitaxel, Docetaxel, polyamines, a proteasome inhibitor, a kinase inhibitor, a signaling peptide, accutin, cidofovir, vincristine, bleomycin, AGM-1470, platelet factor 4 and minocycline.

33. The isolated peptide of claim 30, wherein said cytokine is selected from the group consisting of interleukin 1 (IL-1), IL-2, IL-5, IL-10, IL-11, IL-12, IL-18,

interferon-γ (IF-γ), IF-α, IF-ß, tumor necrosis factor-α (TNF-α), or GM-CSF (granulocyte macrophage colony stimulating factor).

34. The isolated peptide of claim 22, wherein said peptide is attached to a macromolecular complex.

35. The isolated peptide of claim 34, wherein said complex is a virus, a bacteriophage, a bacterium, a liposome, a microparticle, a magnetic bead, a yeast cell, a mammalian cell or a cell.

36. The isolated peptide of claim 34, wherein said peptide is attached to a eukaryotic expression vector.

37. The isolated peptide of claim 36, wherein said vector is a gene therapy vector.

38. The isolated peptide of claim 22, wherein said peptide is attached to a solid support.

39. A composition comprising the isolated peptide of claim 22 in a pharmaceutically acceptable carrier.

40. The composition of claim 39, wherein the isolated peptide is attached to a molecule or a macromolecular complex.

41. The isolated peptide of claim 22, wherein said sequence is selected from any of SEQ ID NO:5 through SEQ ID NO:19.

42. The isolated peptide of claim 22, wherein said sequence is selected from any of SEQ ID NO:20 through SEQ ID NO:38.

43. The isolated peptide of claim 22, wherein said sequence is selected from any of SEQ ID NO:210 through SEQ ID NO:234.

44. The isolated peptide of claim 22, wherein said sequence is selected from any of SEQ ID NO:56 through SEQ ID NO:68.

45. The isolated peptide of claim 22, wherein said sequence is selected from any of SEQ ID NO:69 through SEQ ID NO:88.

46. The isolated peptide of claim 22, wherein said sequence is selected from any of SEQ ID NO:235 through SEQ ID NO:250.

47. The isolated peptide of claim 22, wherein said sequence is selected from SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91 or SEQ ID NO:92.

48. A kit comprising the isolated peptide of claim 22 and a control peptide, each in a container.

49. An antibody that selectively binds to an isolated peptide, the peptide comprising at least three contiguous amino acids selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:250.

50. A method comprising;

a) injecting a subject with a phage display library;

b) recovering at least one sample of at least one organ, tissue or cell type;

c) separating the sample into isolated cells or clumps of cells;

d) centrifuging the cells through an organic phase to form a pellet; and

e) recovering phage from the pellet.

51. The method of claim 50, further comprising preselecting the phage display library against a different organ, tissue or cell type.

52. A gene therapy vector, wherein the vector expresses a targeting peptide sequence as part of a surface protein, the targeting peptide comprising at least three contiguous amino acids selected from any of SEQ ID NO:5 through SEQ ID NO:45, SEQ ID NO:47 through SEQ ID NO:121, SEQ ID NO:123 and SEQ ID NO:125 through SEQ ID NO:250.

53. A method of targeting delivery to an organ or tissue, comprising:

a) obtaining a peptide according to claim 22;

b) attaching the peptide to an agent; and

c) administering the agent to a subject.

54. The method of claim 53, wherein the subject is a human or a mouse.

55. The method of claim 53, wherein the agent is a drug, a chemotherapeutic agent, a radioisotope, a pro-apoptosis agent, an anti-angiogenic agent, an enzyme, a hormone, a cytokine, a growth factor, a cytotoxic agent, a peptide, a protein, an antibiotic, an antibody, a Fab fragment of an antibody, an imaging agent, an antigen, a survival factor, an anti-apoptotic agent, a hormone antagonist, a virus, a bacteriophage, a bacterium, a liposome, a microparticle, a magnetic bead, a microdevice, a yeast cell, a mammalian cell, a cell or an expression vector.

56. The method of claim 53, wherein the agent is an imaging agent.

57. The method of claim 56, further comprising obtaining an image of the subject.

58. The method of claim 57, wherein the image is diagnostic for a disease.

59. The method of claim 58, wherein the disease is cancer, arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune disease, bacterial infection, viral infection, cardiovascular disease or degenerative disease.

60. The method of claim 53, wherein the organ or tissue is bone marrow, prostate, prostate cancer, ovary, ureter, placenta, adipose, spleen, angiogenic tissue or ascites.

61. A method of targeting delivery to prostate cancer comprising:

a) obtaining a targeting peptide comprising at least three contiguous amino acids selected from any of SEQ ID NO:20 through SEQ ID NO:38;

b) attaching the peptide to a therapeutic agent to form a complex; and

c) administering the complex to a subject with prostate cancer.

62. A method of diagnosing prostate cancer comprising:

a) obtaining a targeting peptide comprising at least three contiguous amino acids selected from any of SEQ ID NO:20 through SEQ ID NO:38;

b) administering the peptide to a subject suspected of having prostate cancer; and

c) detecting the peptide bound to prostate cancer cells.

63. A method of identifying targeting peptides to angiogenic tissue comprising:

a) inducing hypoxia in a neonatal subject;

b) administering a phage display library to the subject; and

c) recovering phage from the retina of the subject.

64. A method of inducing apoptosis in a cell comprising:

a) obtaining a targeting peptide comprising at least three contiguous amino acids selected from any of SEQ ID NO:93 through SEQ ID NO:121;

b) attaching the peptide to a permeabilizing agent to form a complex; and

c) administering the complex to the cell.

65. The method of claim 64, wherein the permeabilizing agent is selected from a peptide with an amino acid sequence of SEQ ID NO:122 or HIV Tat protein.

66. The method of claim 64, wherein the targeting peptide has the amino acid sequence of SEQ ID NO:112.

67. A method of inducing apoptosis in a cell comprising:

a) attaching Annexin V to a permeabilizing agent to form a complex; and

b) administering the complex to the cell.

68. The method of claim 67, wherein the permeabilizing agent is selected from a peptide with an amino acid sequence of SEQ ID NO:122 or HIV Tat protein

69. A method of modulating angiogenesis comprising:

a) obtaining a peptide comprising at least three contiguous amino acids selected from SEQ ID NO:93 through SEQ ID NO:131; and

b) administering the peptide to a subject.

70. The method of claim 69 wherein the subject has a tumor and the peptide inhibits tumor growth or survival.

71. The method of claim 69, wherein the peptide is attached to an agent.

72. The method of claim 71, wherein the agent is thrombospondin, angiostatin5, pigment epithelium-drived factor, angiotensin, laminin peptides, fibronectin

peptides, plasminogen activator inhibitors, tissue metalloproteinase inhibitors, interferons, interleukin 12, platelet factor 4, IP-10, Gro-ß, thrombospondin, 2-methoxyoestradiol, proliferin-related protein, carboxiamidotriazole, CM101, Marimastat, pentosan polysulphate, angiopoietin 2 (Regeneron), interferon-alpha, herbimycin A, PNU145156E, 16K prolactin fragment, Linomide, thalidomide, pentoxifylline, genistein, TNP-470, endostatin, paclitaxel, accutin, cidofovir, vincristine, bleomycin, AGM-1470, platelet factor 4 or minocycline.

73. The method of claim 69, wherein the peptide has anti-angiogenic activity.

74. The method of claim 69, wherein the peptide has pro-angiogenic activity.

75. The method of claim 73, further comprising administering the peptide to a subject with ischemia.

76. The method of claim 73, further comprising administering the peptide to a subject with cardiovascular disease.

77. The method of claim 69, further comprising administering the peptide to a subject with cancer, arthritis, diabetes, cardiovascular disease, inflammation or macular degeneration.

78. A method of targeting delivery to an angiogenic tissue comprising:

a) obtaining a peptide comprising at least three contiguous amino acids selected from SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130 or SEQ ID NO:131;

b) attaching the peptide to a therapeutic agent to form a complex; and

b) administering the complex to a subject.

79. The method of claim 78, wherein the peptide has an amino acid sequence of SEQ ID NO:123.

80. The method of claim 78, wherein the angiogenic tissue is from a subject with cancer, arthritis, diabetes, cardiovascular disease, inflammation or macular degeneration.

81. A method of detecting receptors for endostatin or angiostatin comprising

a) obtaining a sample from a tissue or organ;

b) incubating the sample with endostatin or angiostatin; and

c) detecting the presence of endostatin or angiostatin bound to the sample.

82. The method of claim 81, wherein the sample is a thin section of a tissue or organ.

83. The method of claim 82, further comprising assessing specificity by inhibiting binding with a targeting peptide selective for endostatin or angiostatin.

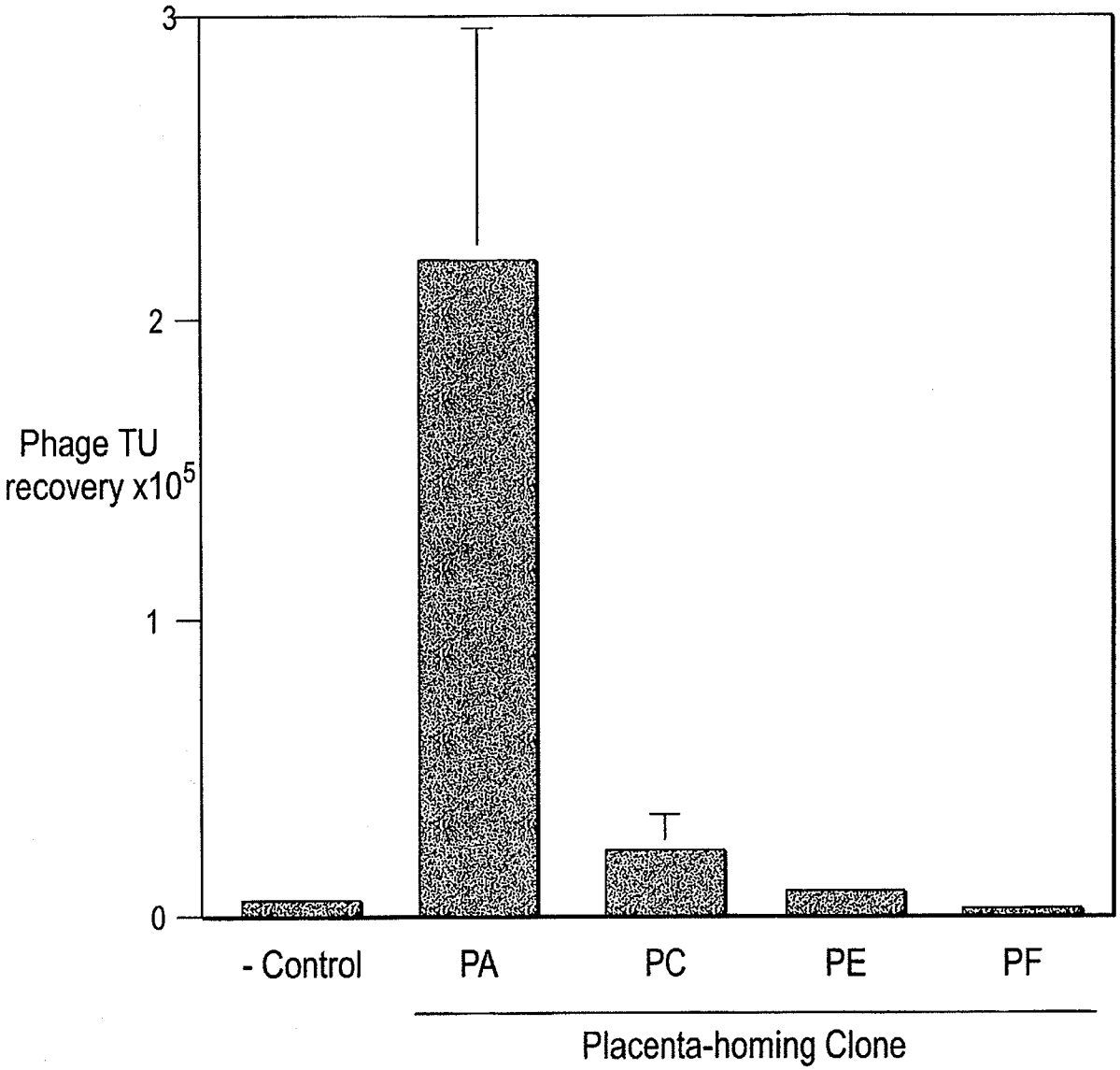
3
2
1
0
Phage TU recovery x10^5
- Control
PA
PC
PE
PF
Placenta-homing Clone

Fig. 1

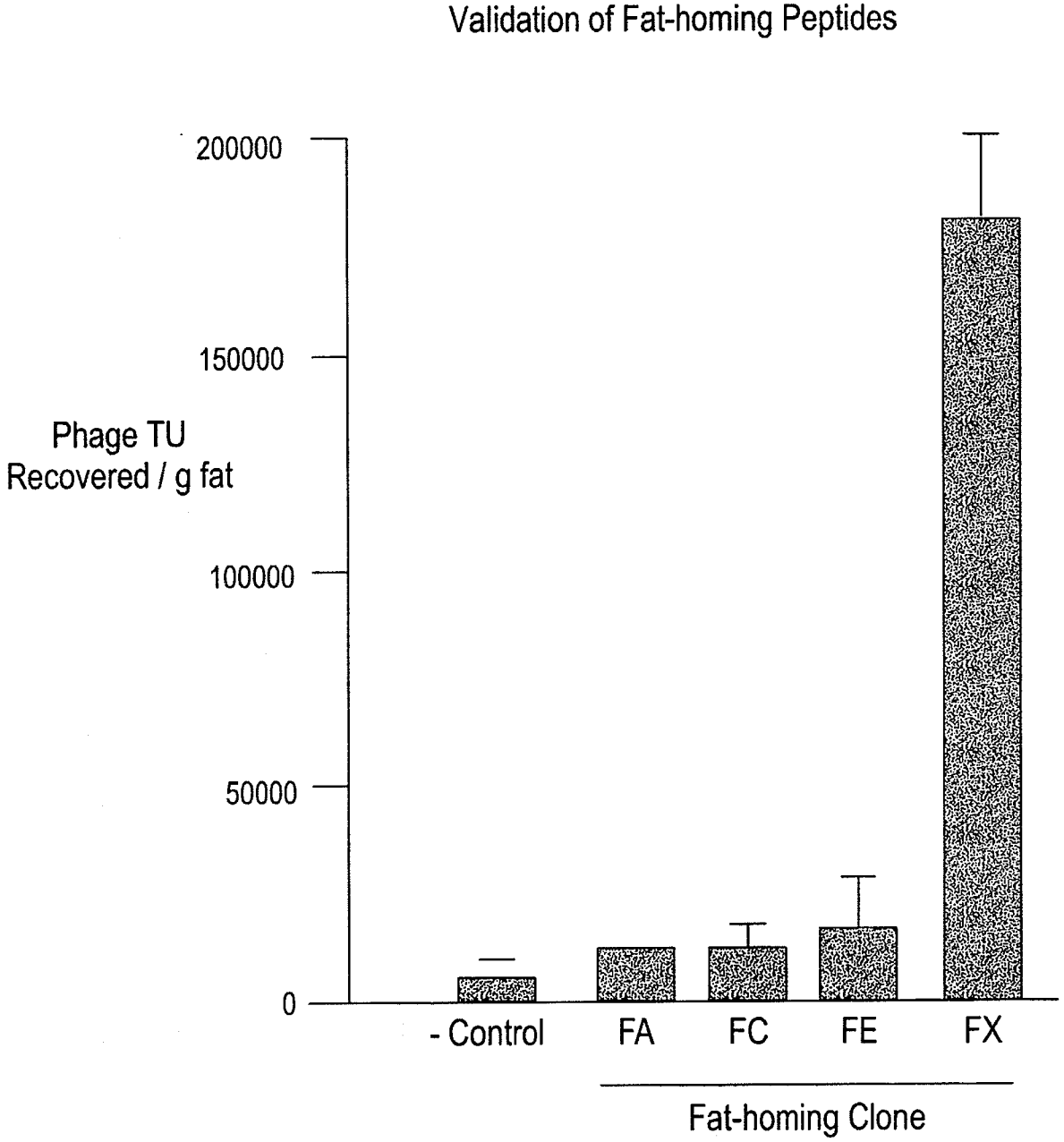
Validation of Fat-homing Peptides
200000
150000
100000
50000
0
Phage TU
Recovered / g fat
- Control
FA
FC
FE
FX
Fat-homing Clone

Fig. 2

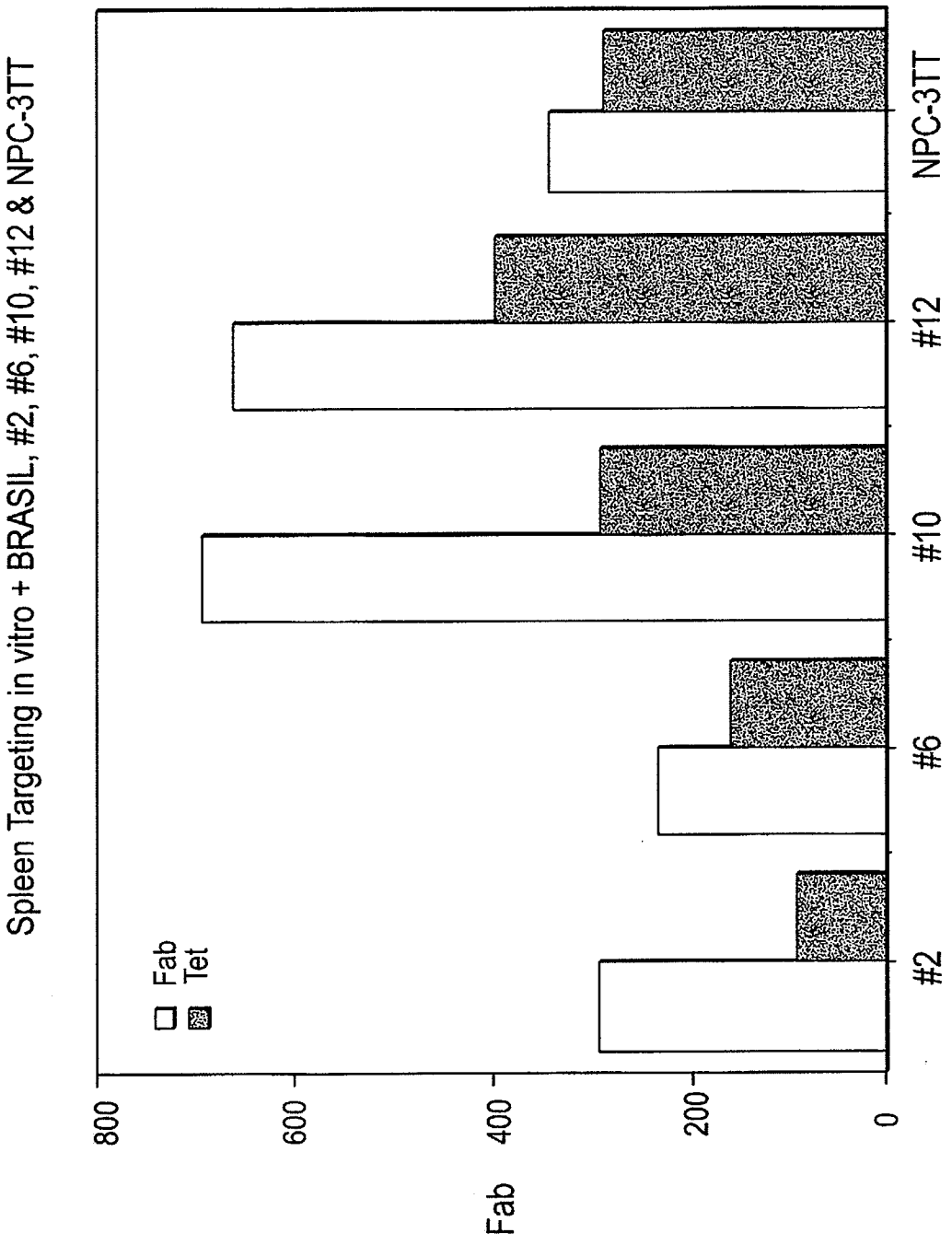
Spleen Targeting in vitro + BRASIL, #2, #6, #10, #12 & NPC-3TT
Fab
Tet
Fab
800
600
400
200
0
#2
#6
#10
#12
NPC-3TT

Fig. 3

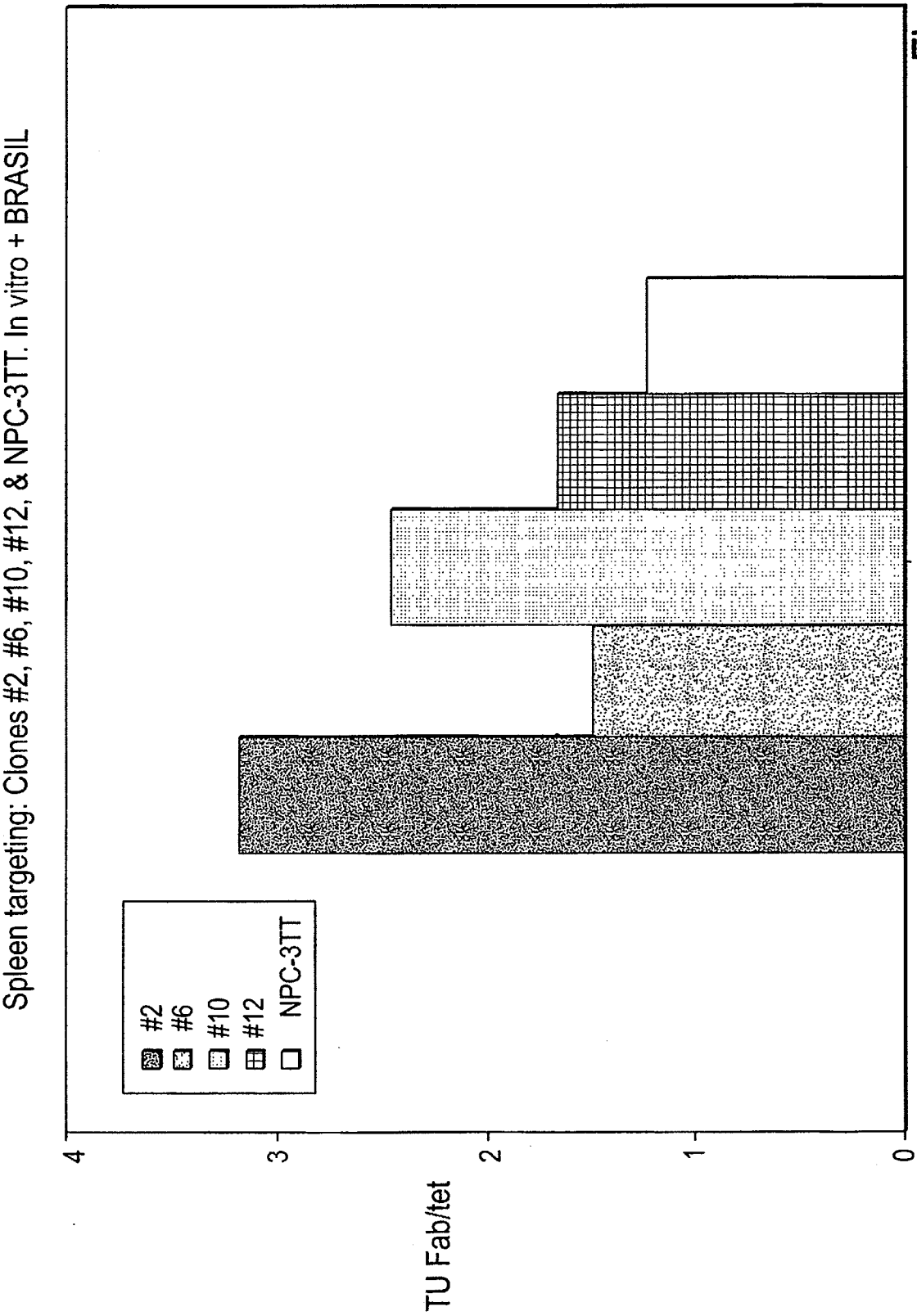
Spleen targeting: Clones #2, #6, #10, #12, & NPC-3TT. In vitro + BRASIL
#2
#6
#10
#12
NPC-3TT
TU Fab/tet
0
1
2
3
4

Fig. 4

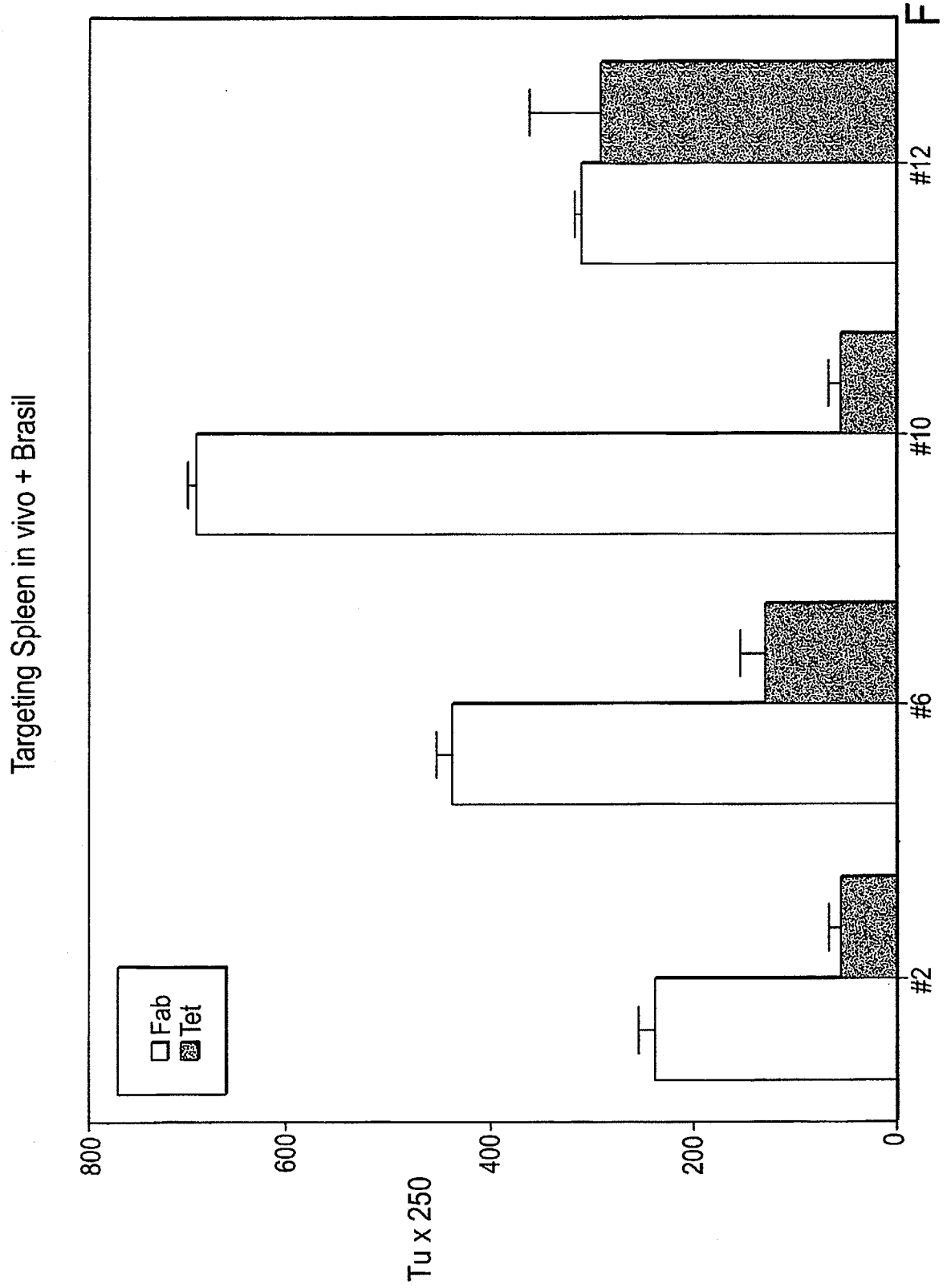
Targeting Spleen in vivo + Brasil
Tu x 250
800
600
400
200
0
Fab
Tet
#2
#6
#10
#12

Fig. 5

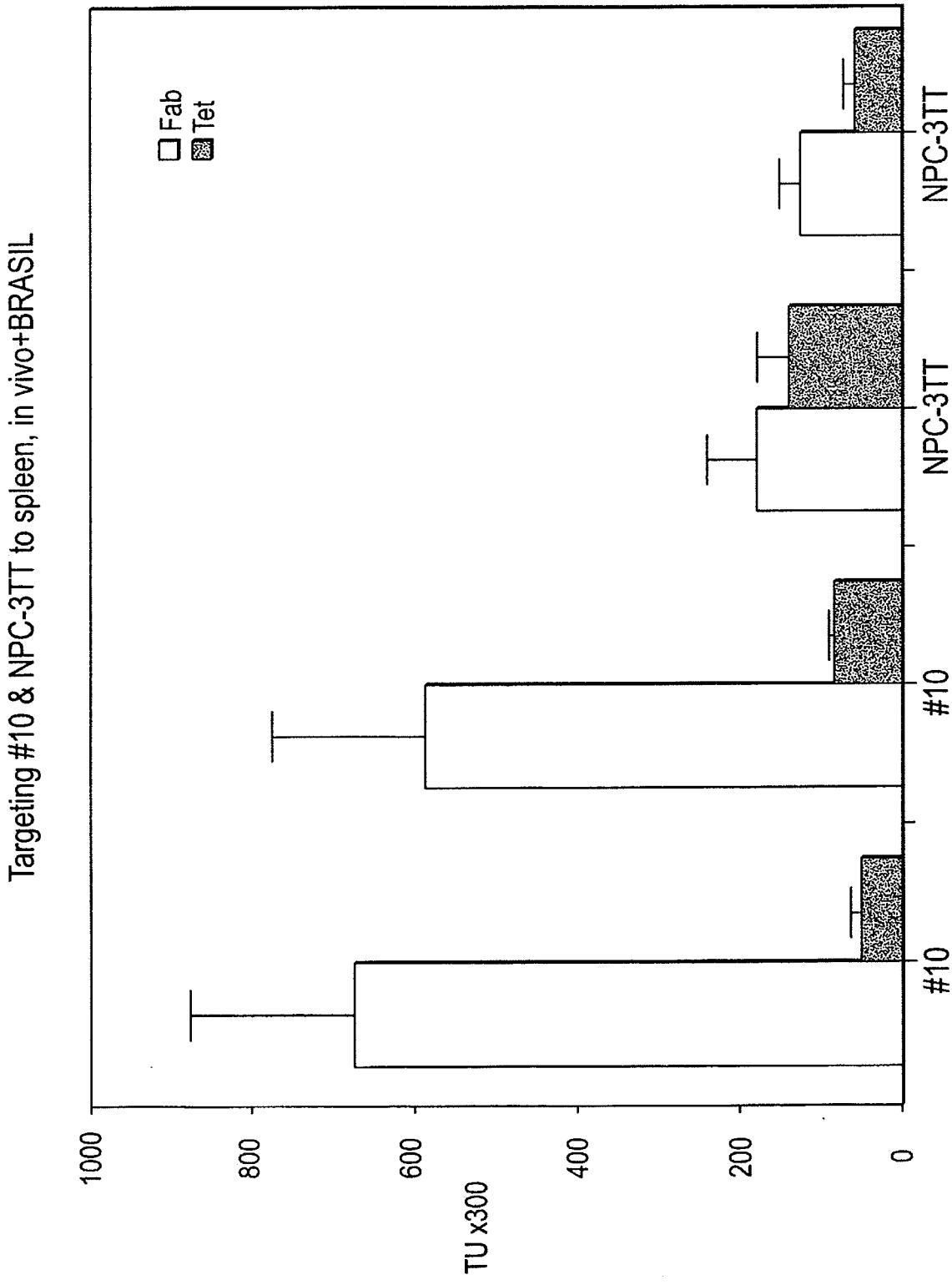
Targeting #10 & NPC-3TT to spleen, in vivo+BRASIL
Fab
Tet
TU x300
1000
800
600
400
200
0
#10
#10
NPC-3TT
NPC-3TT

Fig. 6

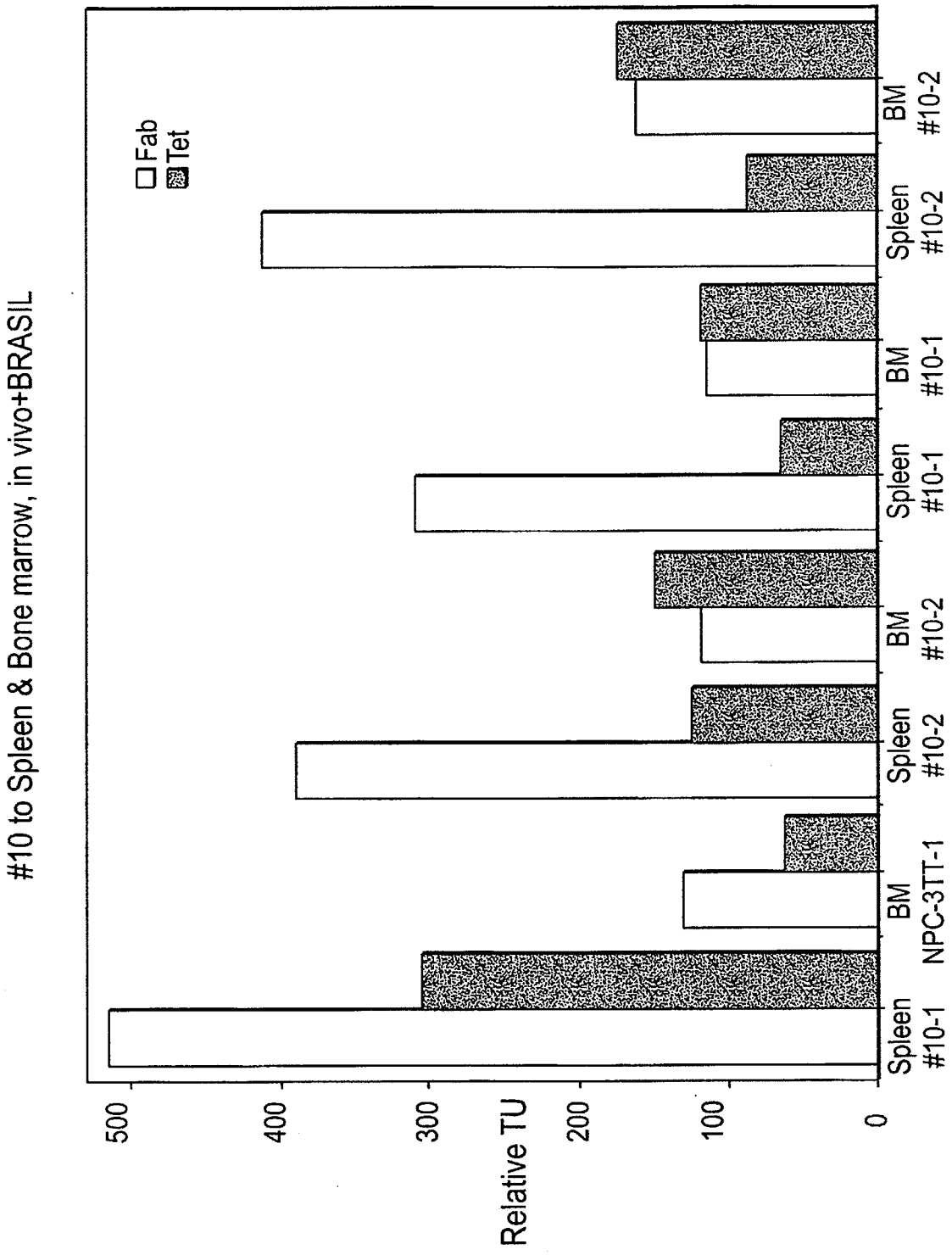
#10 to Spleen & Bone marrow, in vivo+BRASIL
Fab
Tet
Relative TU
0
100
200
300
400
500
Spleen #10-1
BM NPC-3TT-1
Spleen #10-2
BM #10-2
Spleen #10-1
BM #10-1
Spleen #10-2
BM #10-2

Fig. 7

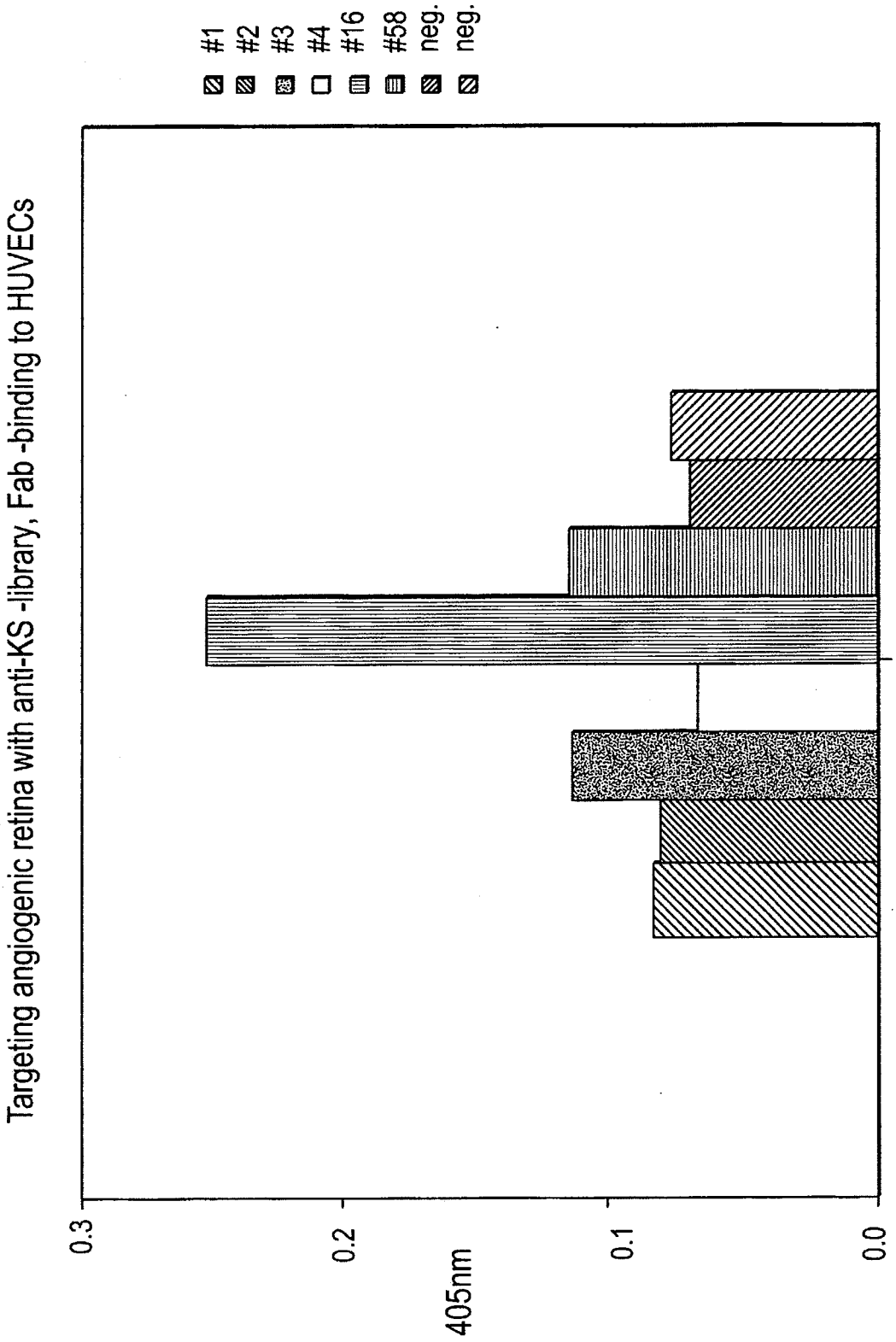
#1
#2
#3
#4
#16
#58
neg.
neg.
Targeting angiogenic retina with anti-KS -library, Fab -binding to HUVECs
0.3
0.2
0.1
0.0
405nm

Fig. 8

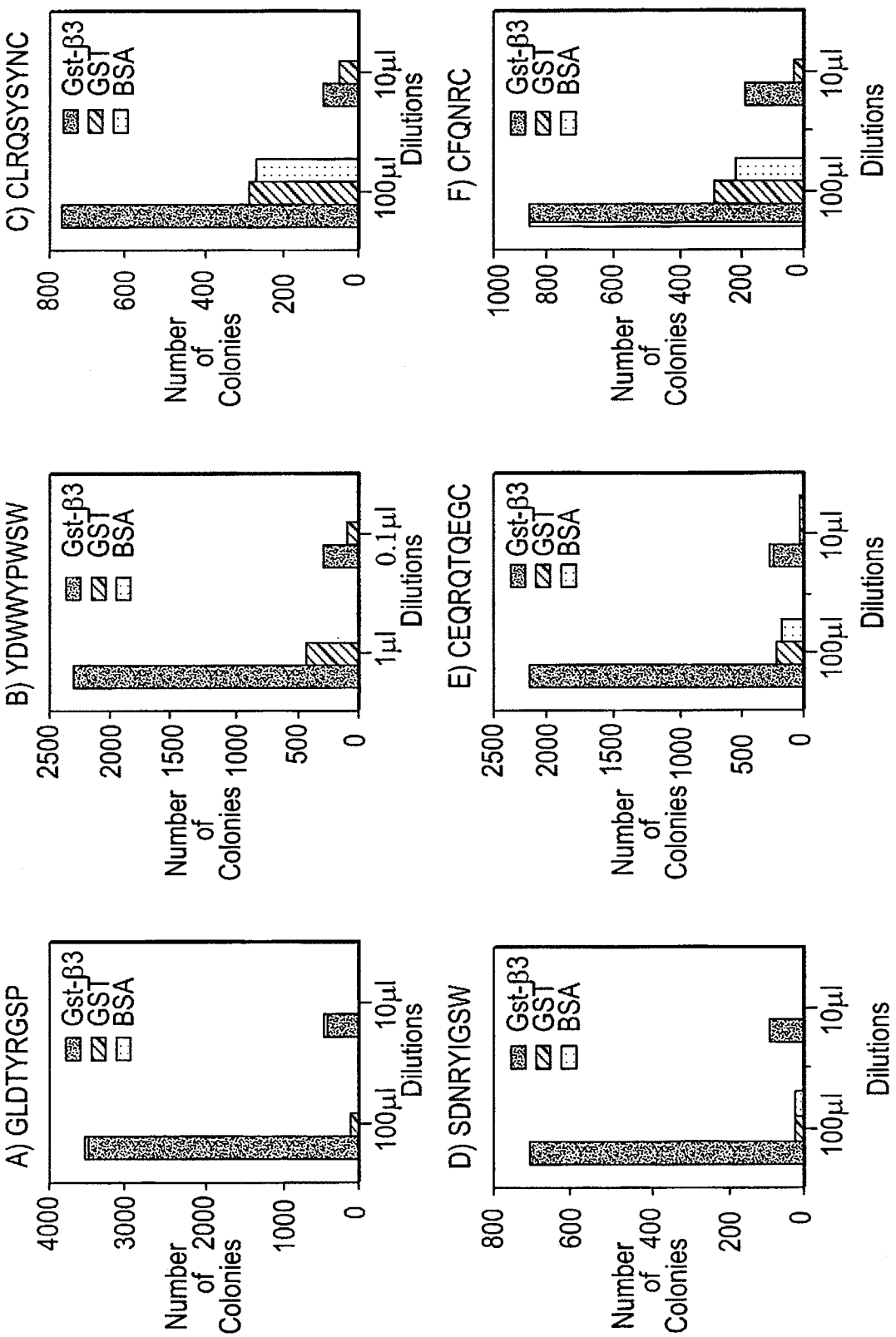
A) GLDTYRGSP
B) YDWWYPWSW
C) CLRQSYSYNC
D) SDNRYIGSW
E) CEQRQTQEGC
F) CFQNRC
Gst-β3
GST
BSA
Number of Colonies
Dilutions
100µl
10µl
1µl
0.1µl

Fig. 9

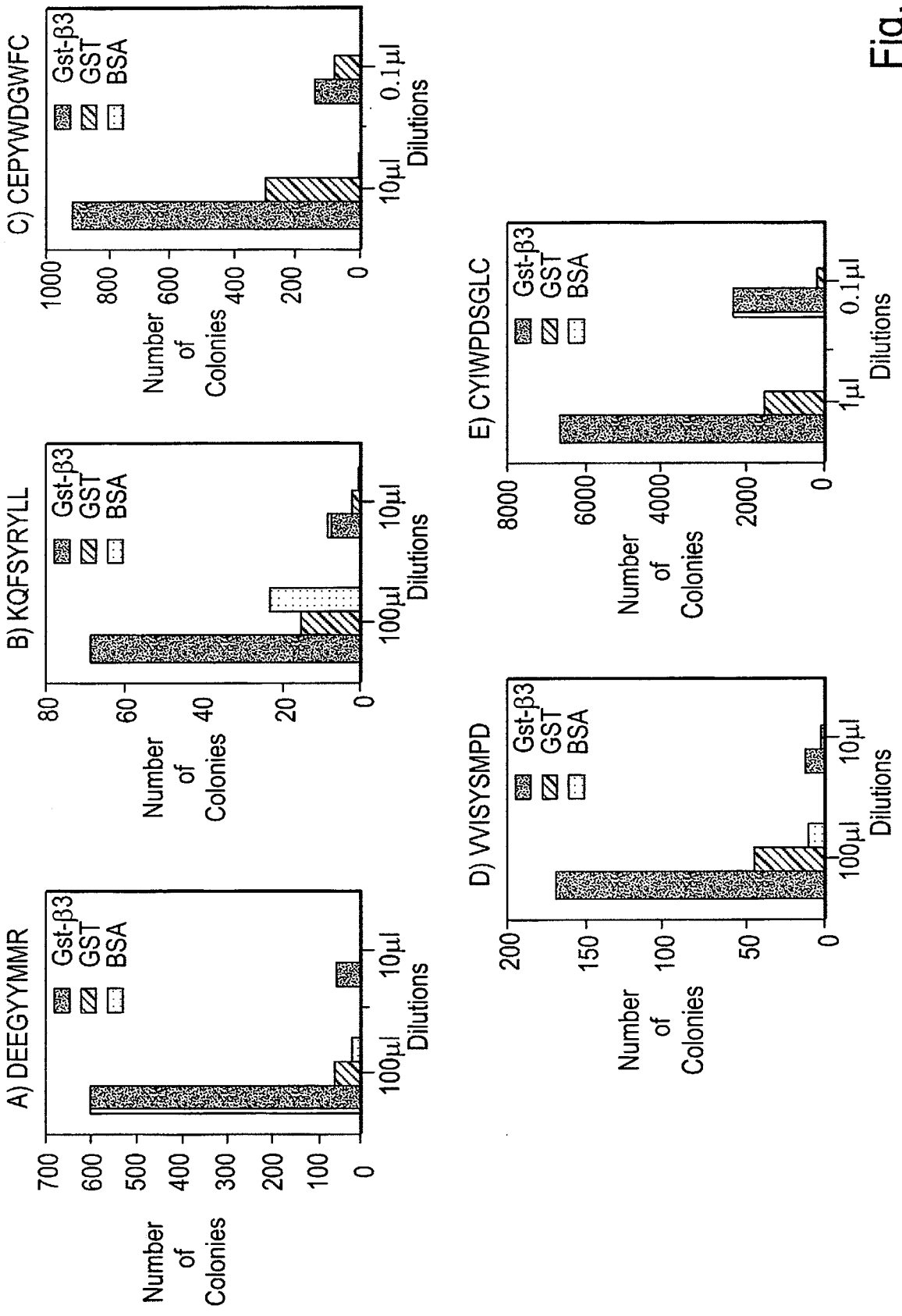
A) DEEGYYMMR
B) KQFSYRYLL
C) CEPYWDGWFC
D) VVISYSMPD
E) CYIWPDSGLC
Gst-β3
GST
BSA
Number of Colonies
Dilutions
100µl
10µl
1µl
0.1µl

Fig. 10

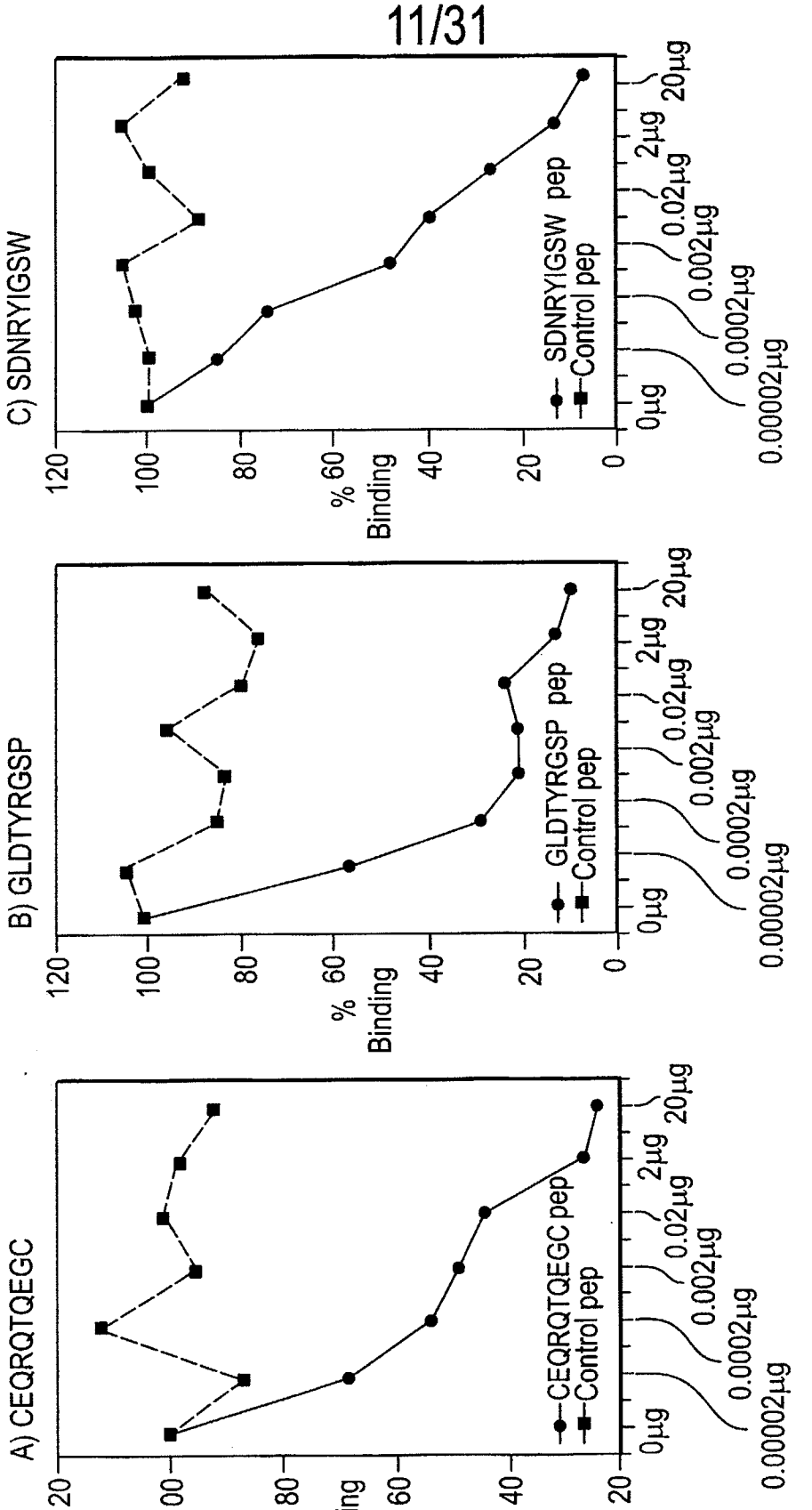
A) CEQRQTQEGC
B) GLDTYRGSP
C) SDNRYIGSW
% Binding
120
100
80
60
40
20
0
CEQRQTQEGC pep
Control pep
GLDTYRGSP pep
Control pep
SDNRYIGSW pep
Control pep
0µg
0.00002µg
0.0002µg
0.002µg
0.02µg
2µg
20µg
Peptide Concentration (µg/well)

Fig. 11

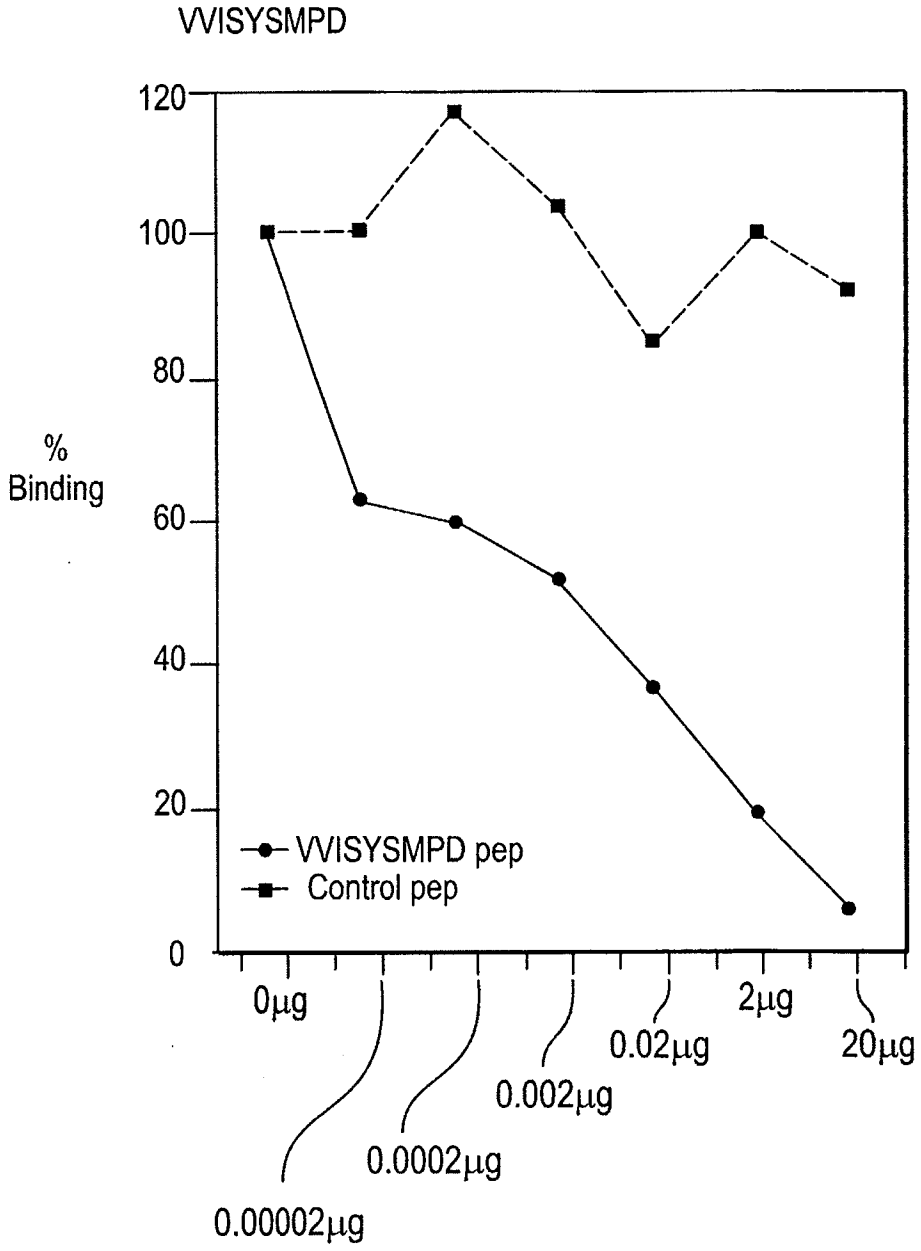
VVISYSMPD
120
100
80
60
40
20
0
% Binding
VVISYSMPD pep
Control pep
0μg
0.00002μg
0.0002μg
0.002μg
0.02μg
2μg
20μg
Peptide Concentration (μg/well)

Fig. 12

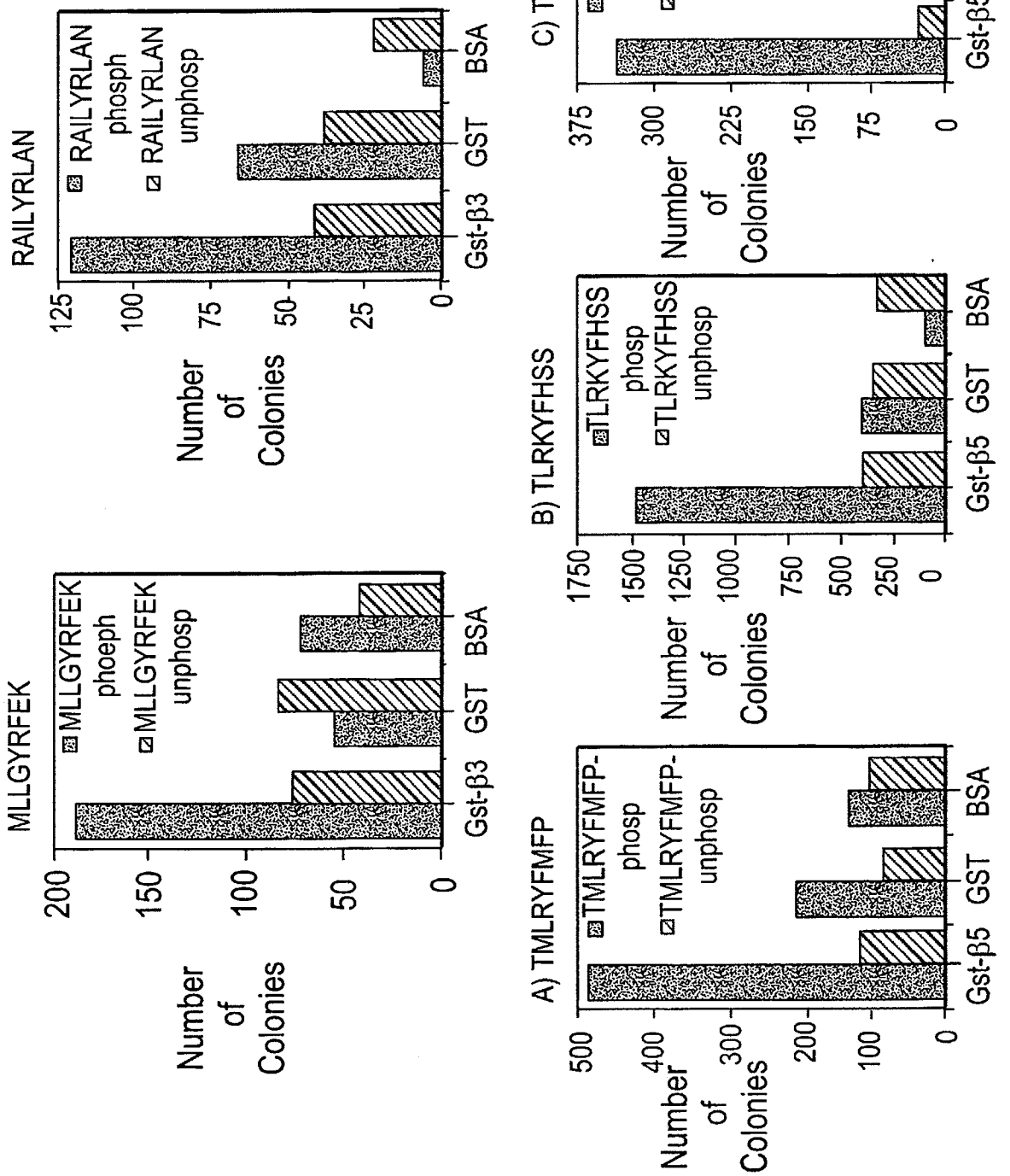
A) TMLRYFMFP
TMLRYFMFP-phosp
TMLRYFMFP-unphosp
Number of Colonies
500
400
300
200
100
0
Gst-β5
GST
BSA
B) TLRKYFHSS
TLRKYFHSS phosp
TLRKYFHSS unphosp
Number of Colonies
1750
1500
1250
1000
750
500
250
0
Gst-β5
GST
BSA
C) TMLRYTVRL
TMLRYTVRL-phosp
TMLRYTVRL-unphosp
Number of Colonies
375
300
225
150
75
0
Gst-β5
GST
BSA
MLLGYRFEK
MLLGYRFEK phoeph
MLLGYRFEK unphosp
Number of Colonies
200
150
100
50
0
Gst-β3
GST
BSA
RAILYRLAN
RAILYRLAN phosph
RAILYRLAN unphosp
Number of Colonies
125
100
75
50
25
0
Gst-β3
GST
BSA

Fig. 13

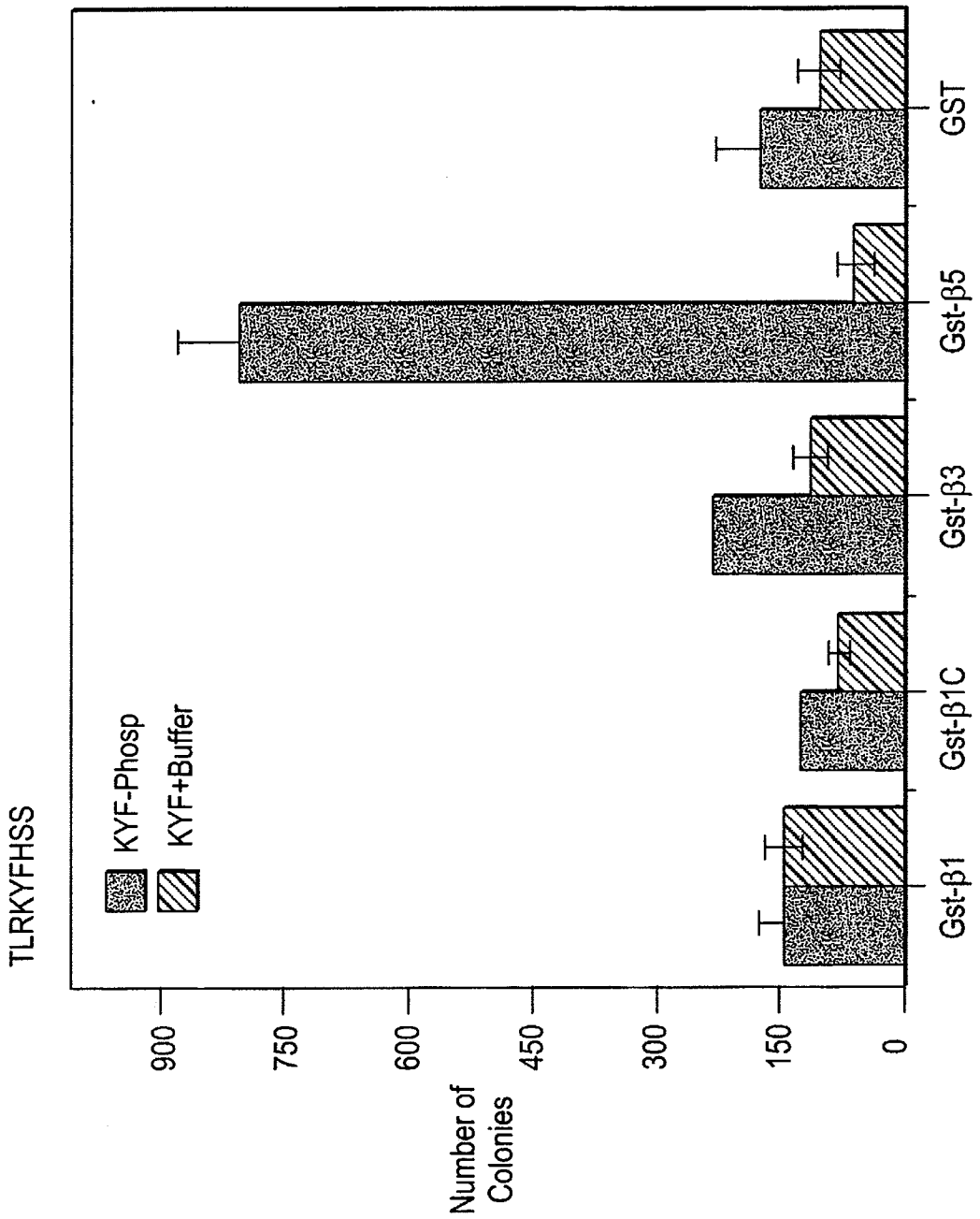
TLRKYFHSS
KYF-Phosp
KYF+Buffer
Number of Colonies
900
750
600
450
300
150
0
Gst-β1
Gst-β1C
Gst-β3
Gst-β5
GST

Fig. 14

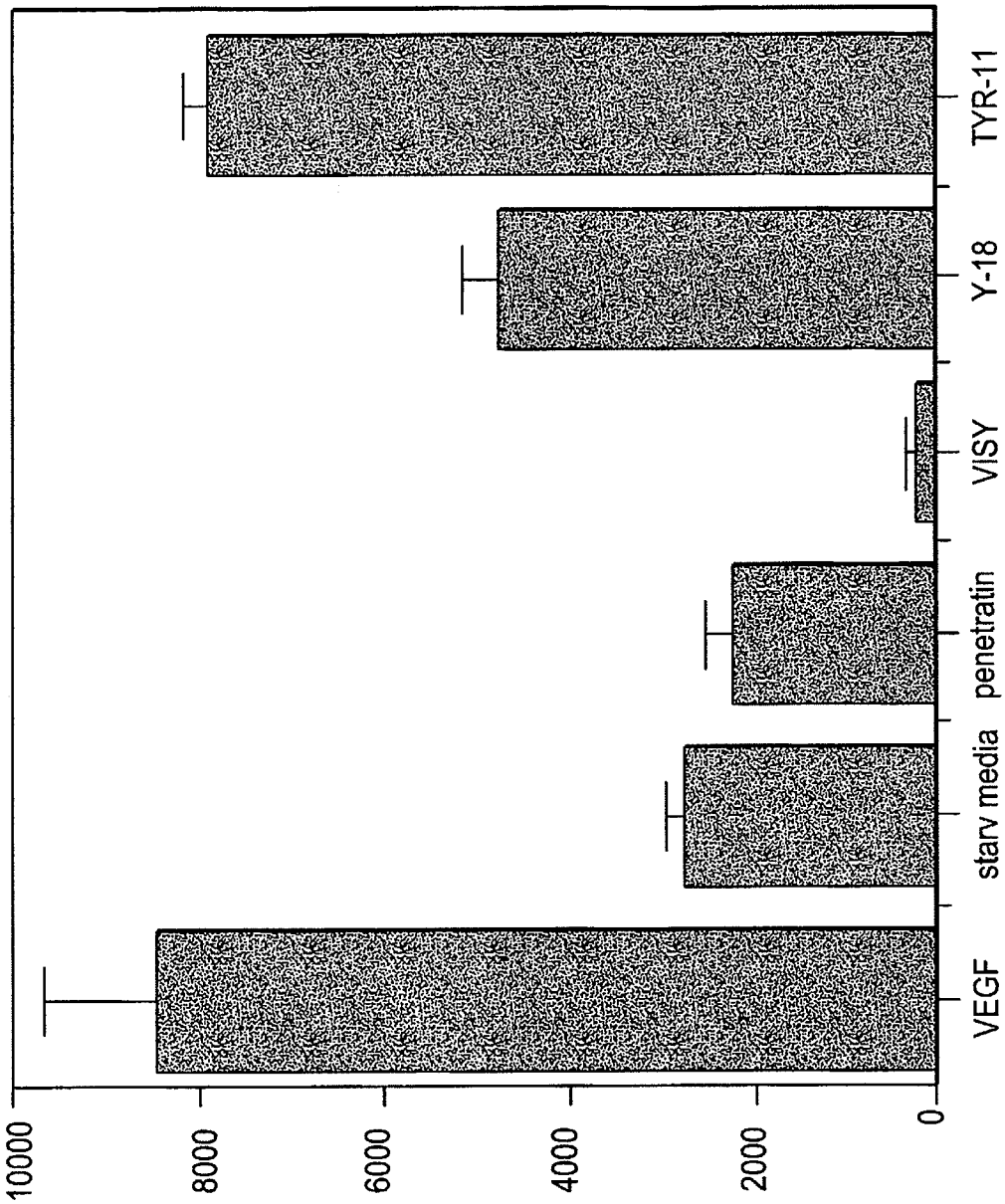
10000
8000
6000
4000
2000
0
VEGF
starv media
penetratin
VISY
Y-18
TYR-11

Fig. 15

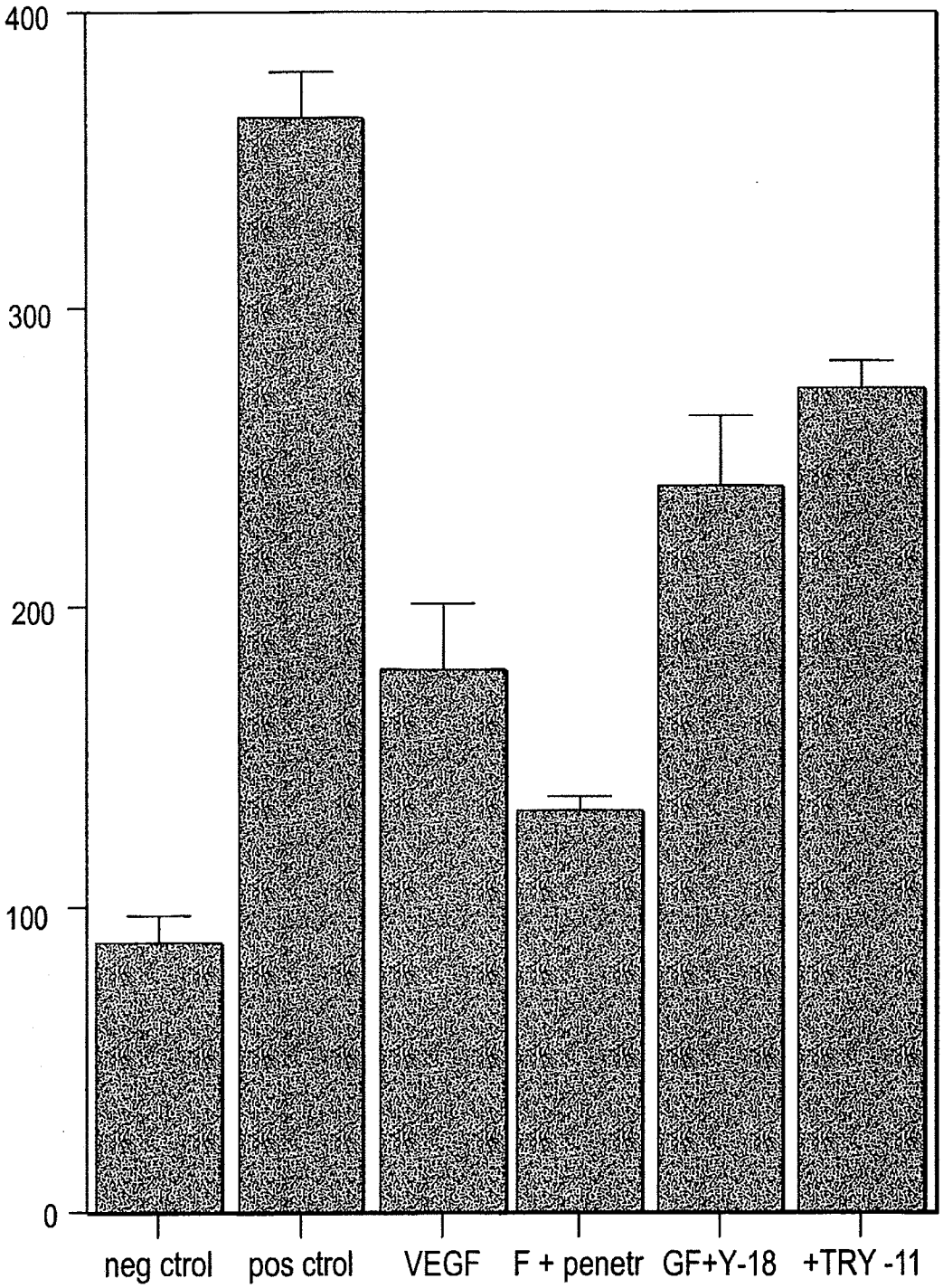
400
300
200
100
0
neg ctrol
pos ctrol
VEGF
F + penetr
GF+Y-18
+TRY -11

Fig. 16

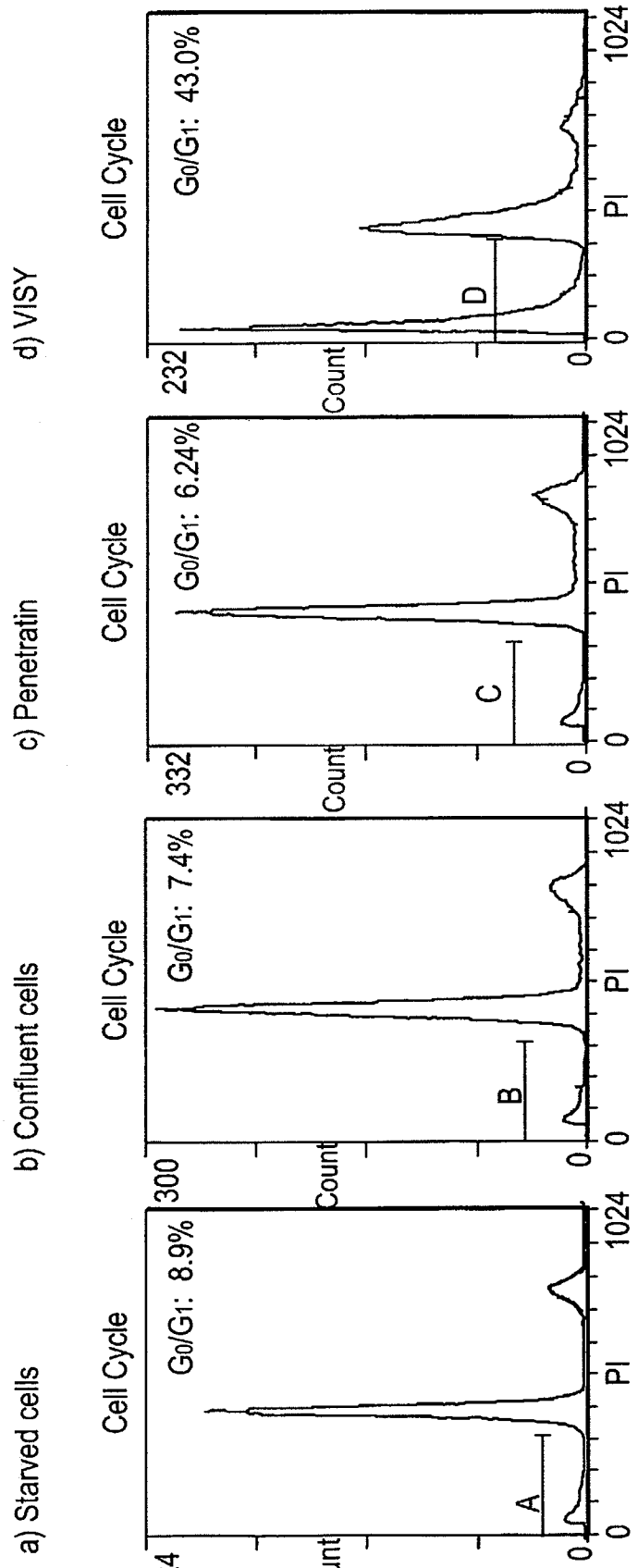
a) Starved cells
b) Confluent cells
c) Penetratin
d) VISY
Cell Cycle
G0/G1: 8.9%
G0/G1: 7.4%
G0/G1: 6.24%
G0/G1: 43.0%
Count
PI
424
300
332
232
0
1024
A
B
C
D

Fig. 17

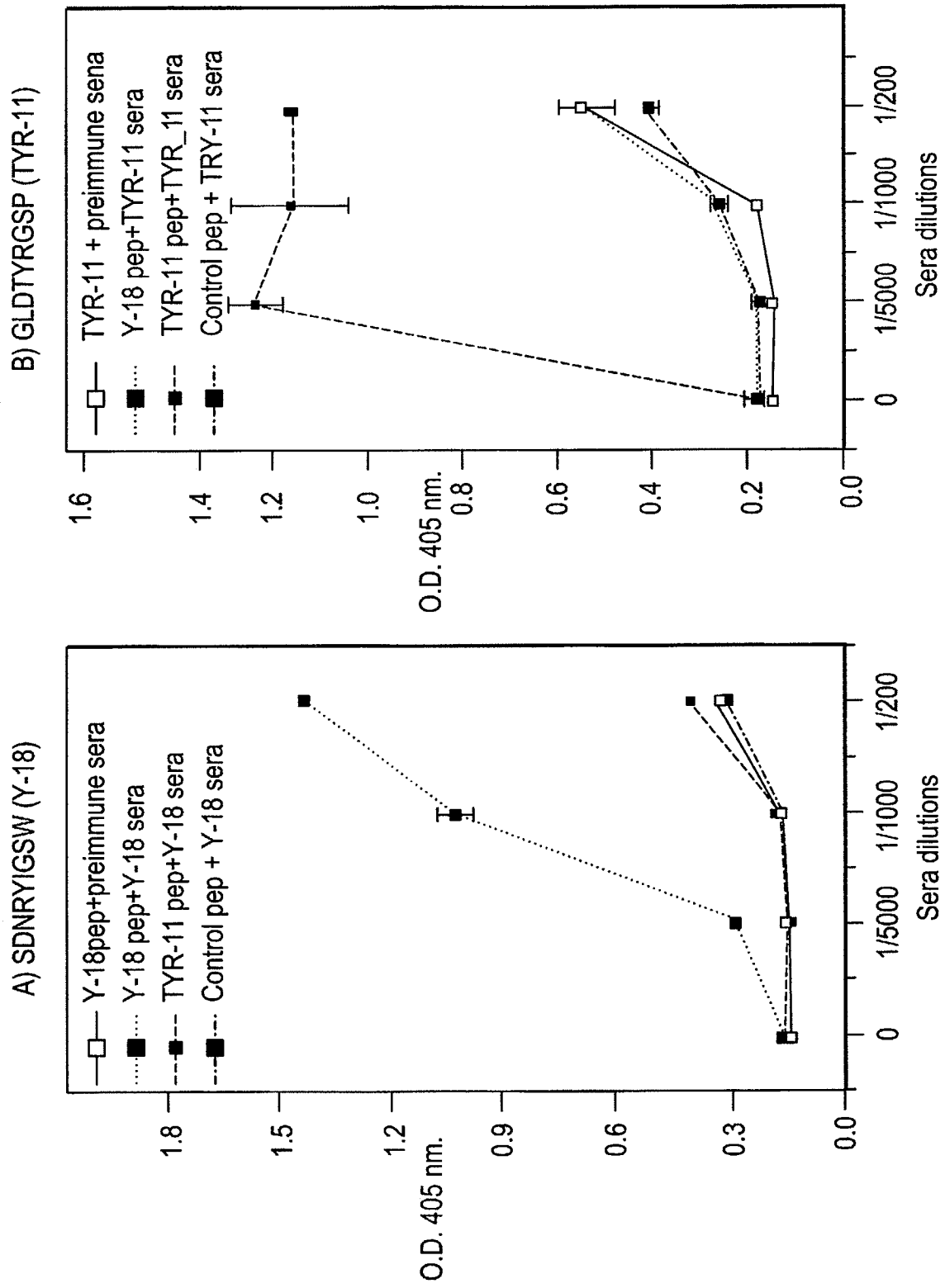
A) SDNRYIGSW (Y-18)
Y-18pep+preimmune sera
Y-18 pep+Y-18 sera
TYR-11 pep+Y-18 sera
Control pep + Y-18 sera
O.D. 405 nm.
1.8
1.5
1.2
0.9
0.6
0.3
0.0
0
1/5000
1/1000
1/200
Sera dilutions
B) GLDTYRGSP (TYR-11)
TYR-11 + preimmune sena
Y-18 pep+TYR-11 sera
TYR-11 pep+TYR_11 sera
Control pep + TRY-11 sera
O.D. 405 nm.
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0
1/5000
1/1000
1/200
Sera dilutions

Fig. 18

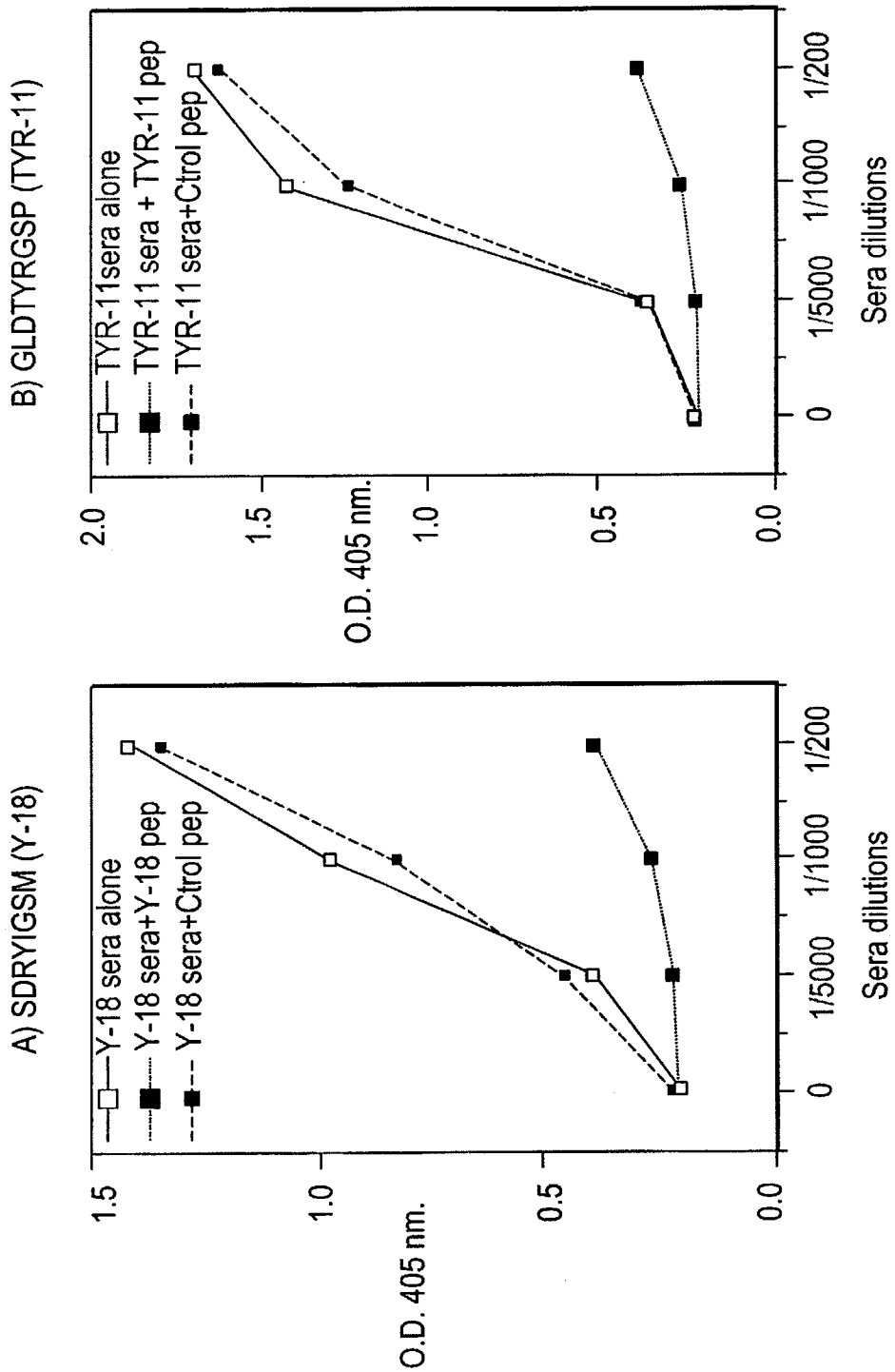
A) SDRYIGSM (Y-18)
Y-18 sera alone
Y-18 sera+Y-18 pep
Y-18 sera+Ctrol pep
O.D. 405 nm.
1.5
1.0
0.5
0.0
0
1/5000
1/1000
1/200
Sera dilutions
B) GLDTYRGSP (TYR-11)
TYR-11sera alone
TYR-11 sera + TYR-11 pep
TYR-11 sera+Ctrol pep
O.D. 405 nm.
2.0
1.5
1.0
0.5
0.0
0
1/5000
1/1000
1/200
Sera dilutions

Fig. 19

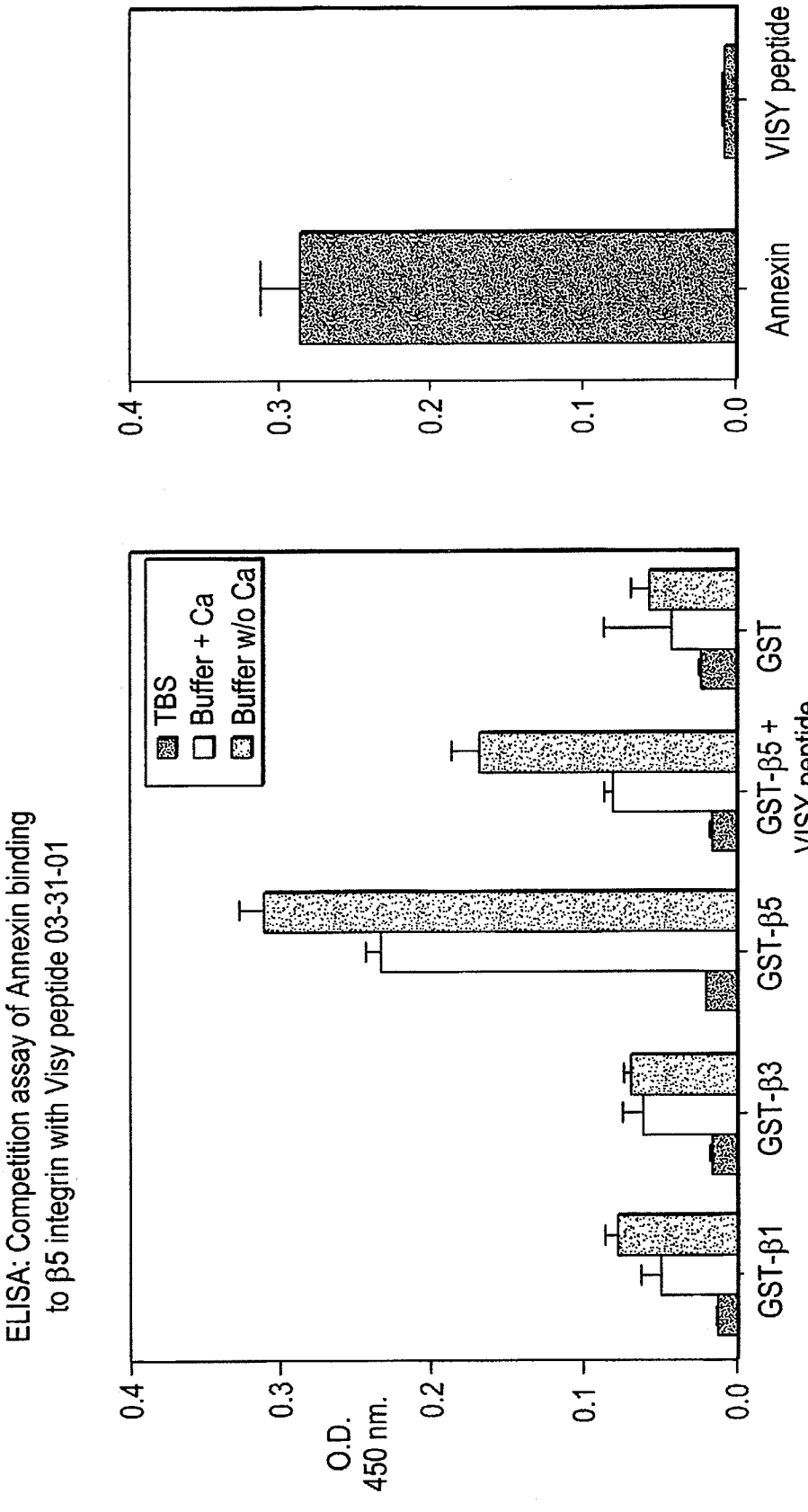
ELISA: Competition assay of Annexin binding
to β5 integrin with Visy peptide 03-31-01
O.D.
450 nm.
0.4
0.3
0.2
0.1
0.0
TBS
Buffer + Ca
Buffer w/o Ca
GST-β1
GST-β3
GST-β5
GST-β5 +
VISY peptide
GST
Annexin
VISY peptide

Fig. 20

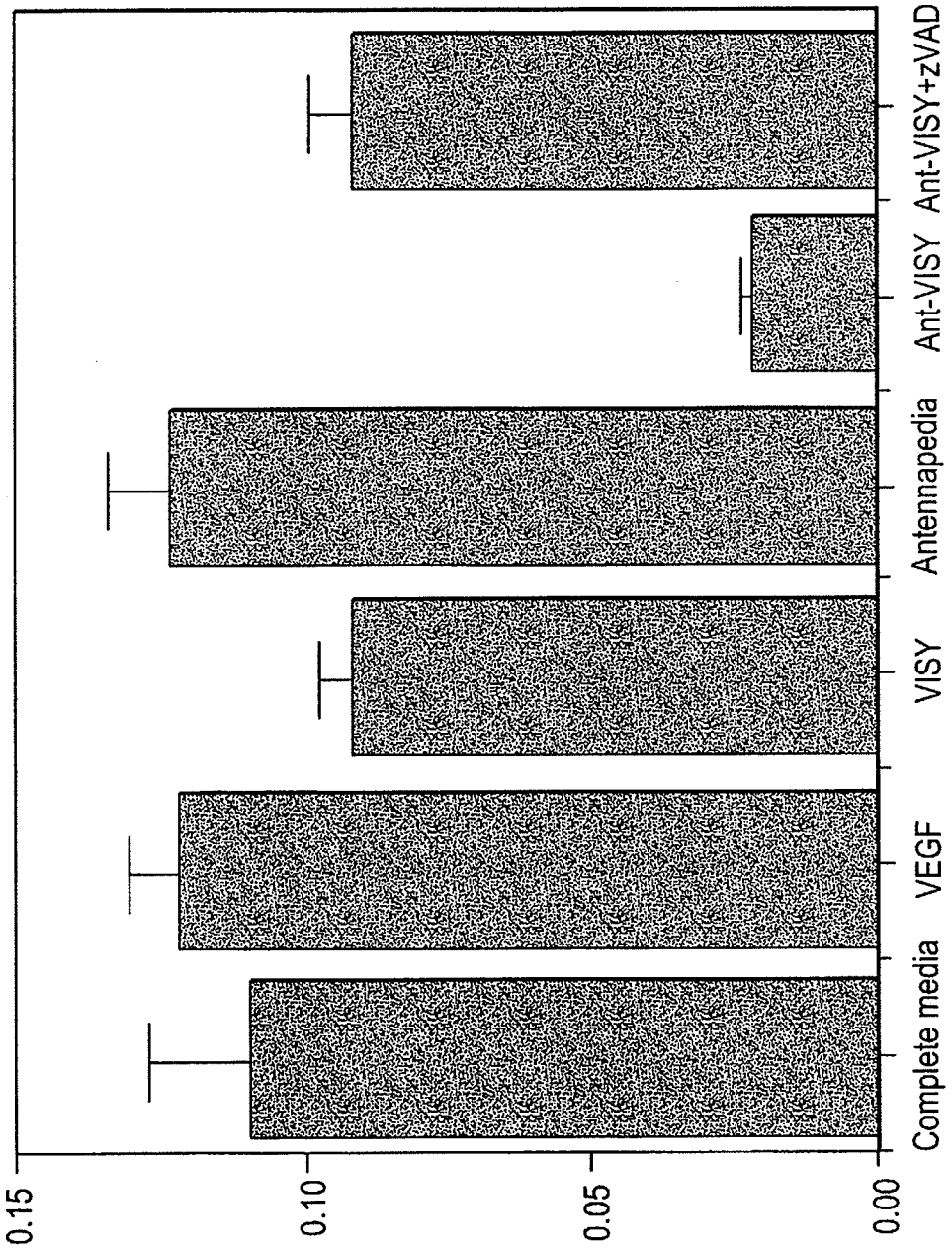
0.15
0.10
0.05
0.00
Complete media
VEGF
VISY
Antennapedia
Ant-VISY
Ant-VISY+zVAD

Fig. 21

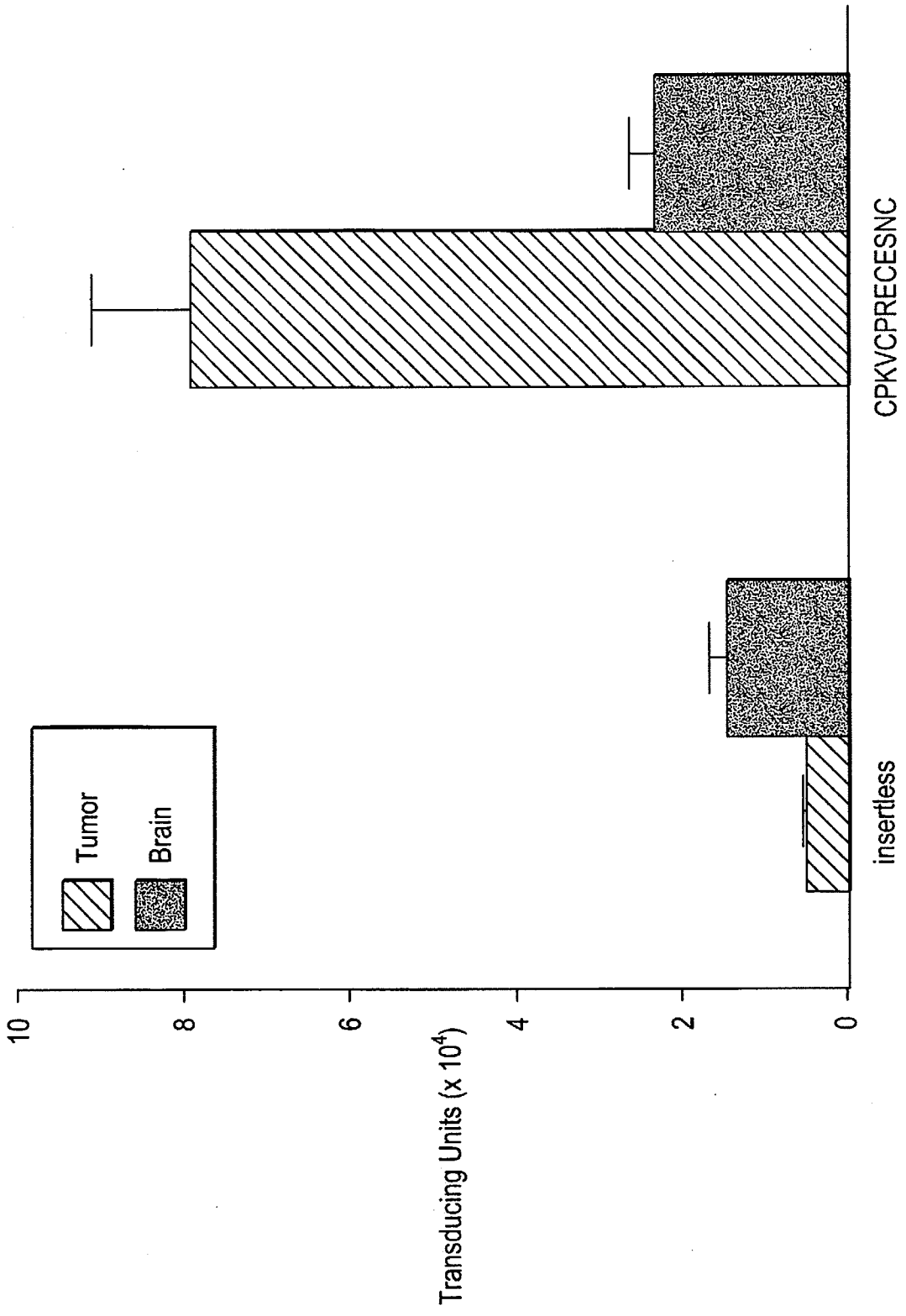
Transducing Units (x 10^4)
10
8
6
4
2
0
Tumor
Brain
insertless
CPKVCPRECESNC

Fig. 22

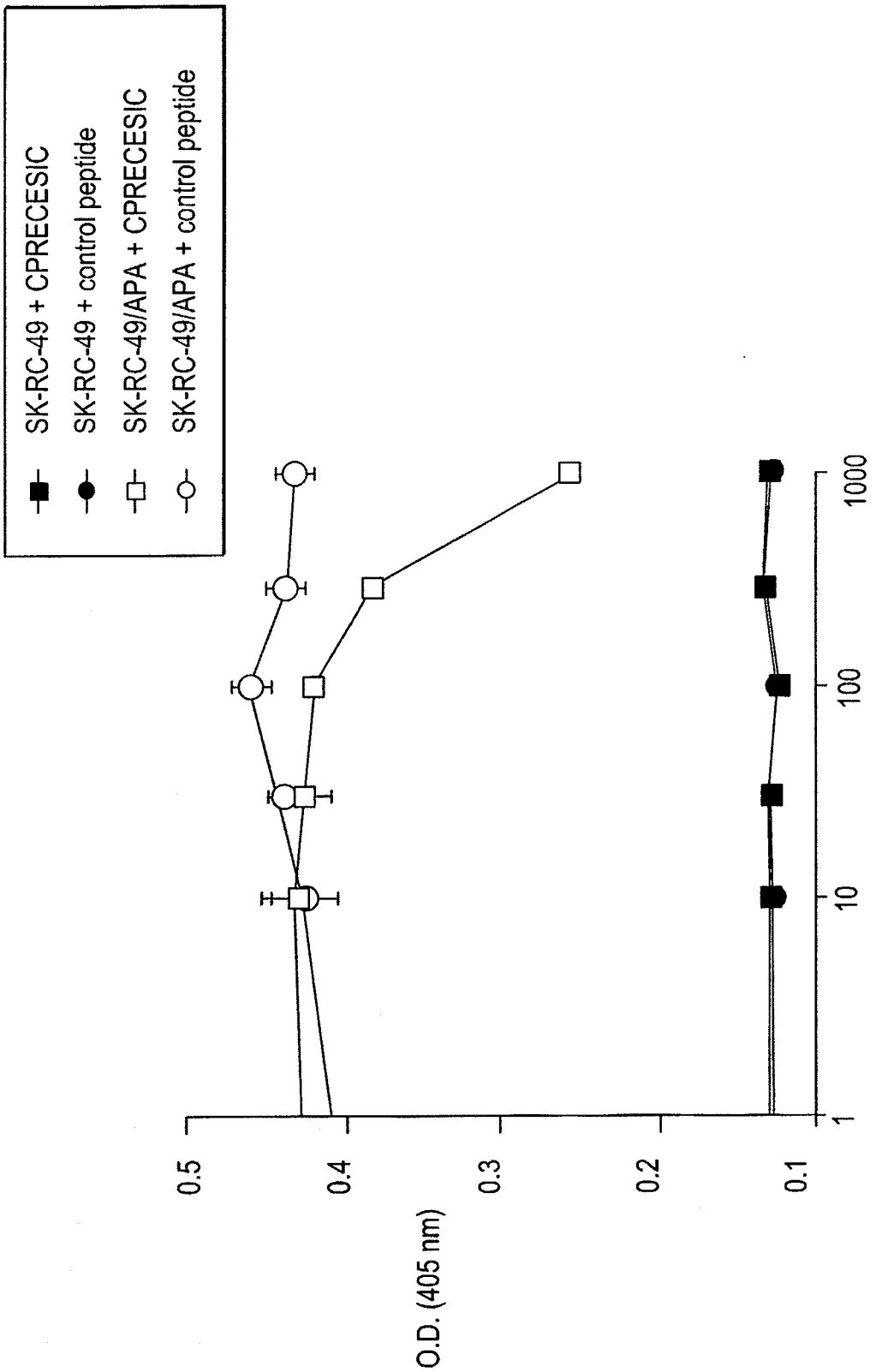
SK-RC-49 + CPRECESIC
SK-RC-49 + control peptide
SK-RC-49/APA + CPRECESIC
SK-RC-49/APA + control peptide
O.D. (405 nm)
0.5
0.4
0.3
0.2
0.1
1
10
100
1000
Peptide concentration (µg/ml)

Fig. 23

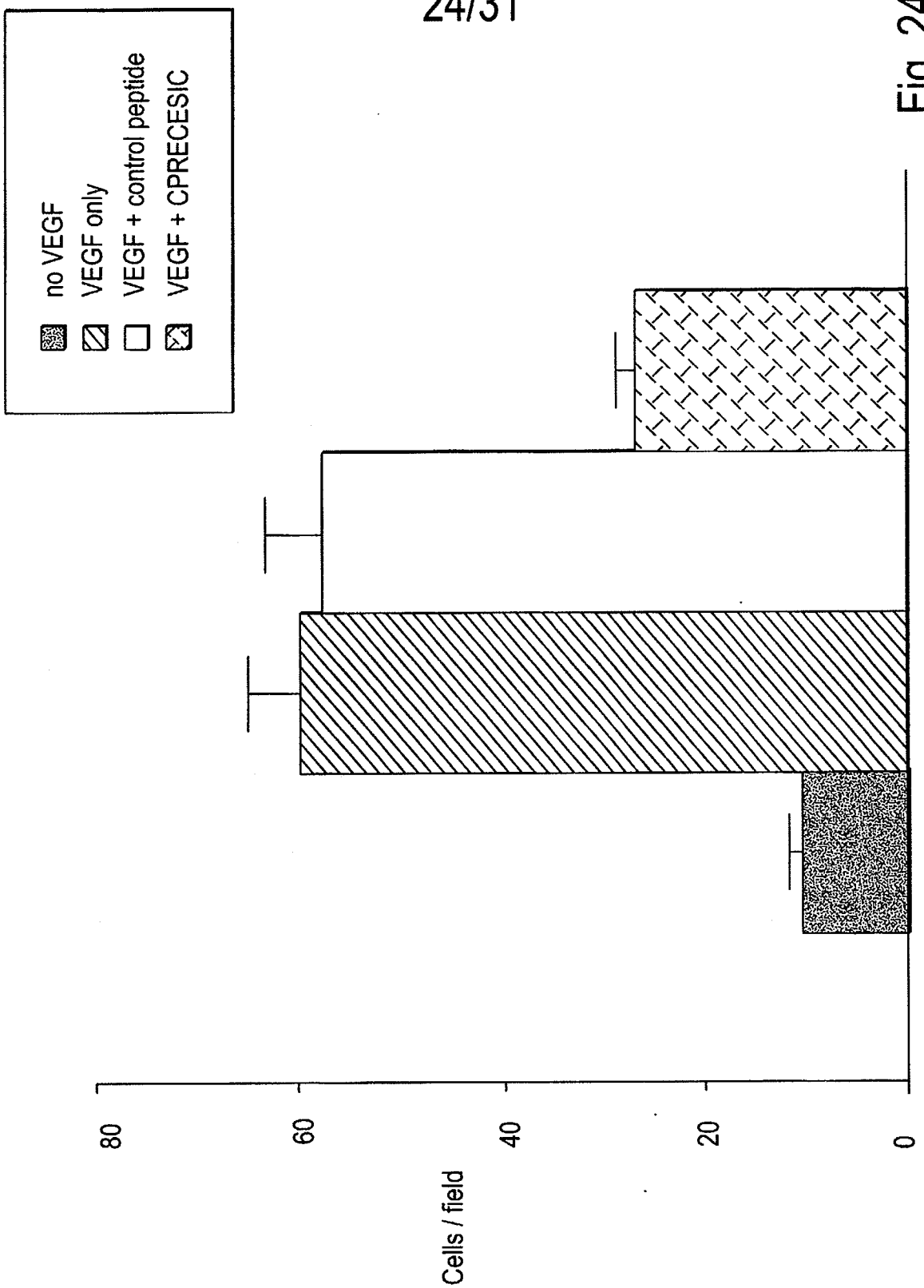
no VEGF
VEGF only
VEGF + control peptide
VEGF + CPRECESIC
Cells / field
0
20
40
60
80

Fig. 24

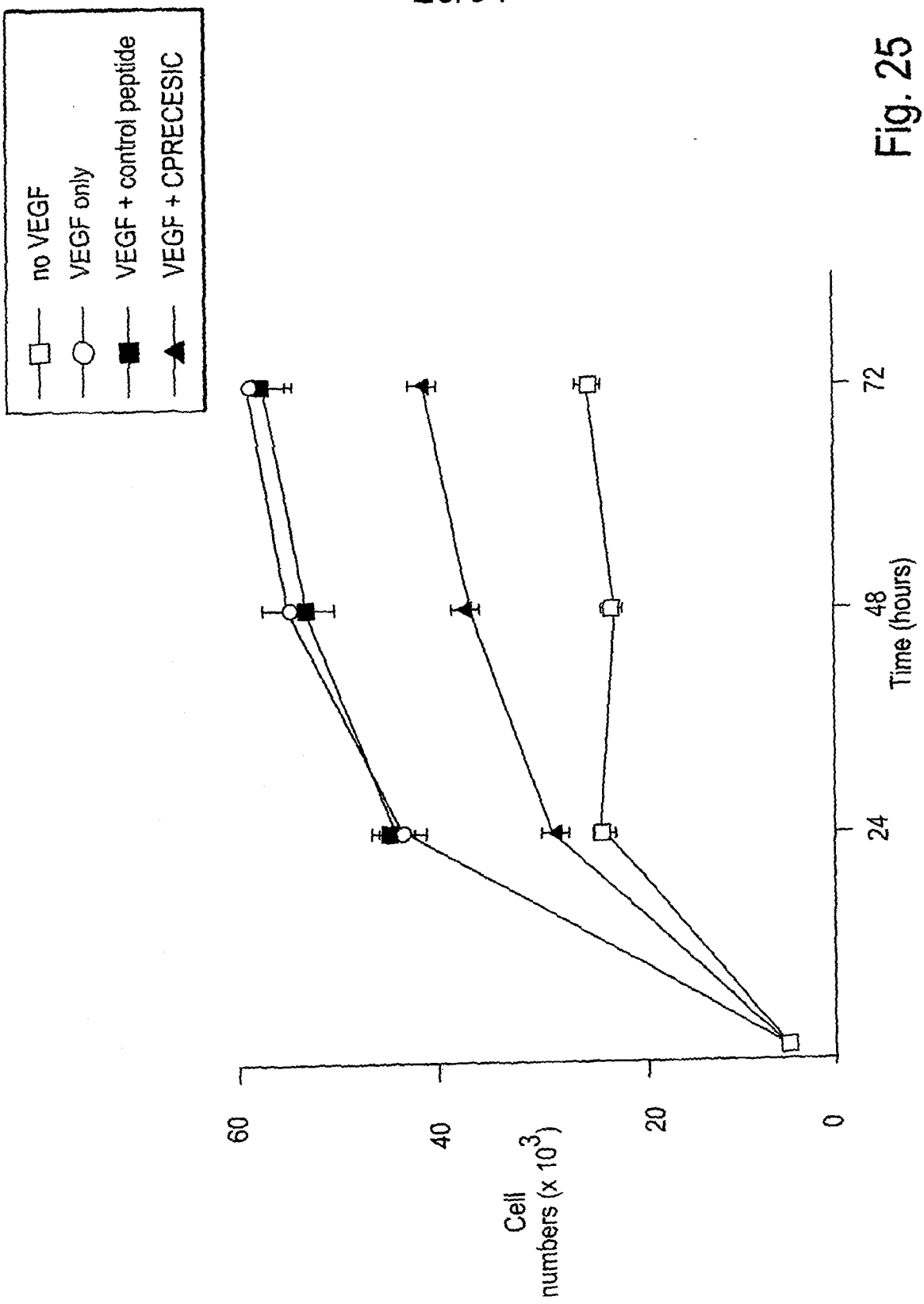
no VEGF
VEGF only
VEGF + control peptide
VEGF + CPRECESIC
Cell numbers (x 10^3)
0
20
40
60
24
48
72
Time (hours)

Fig. 25

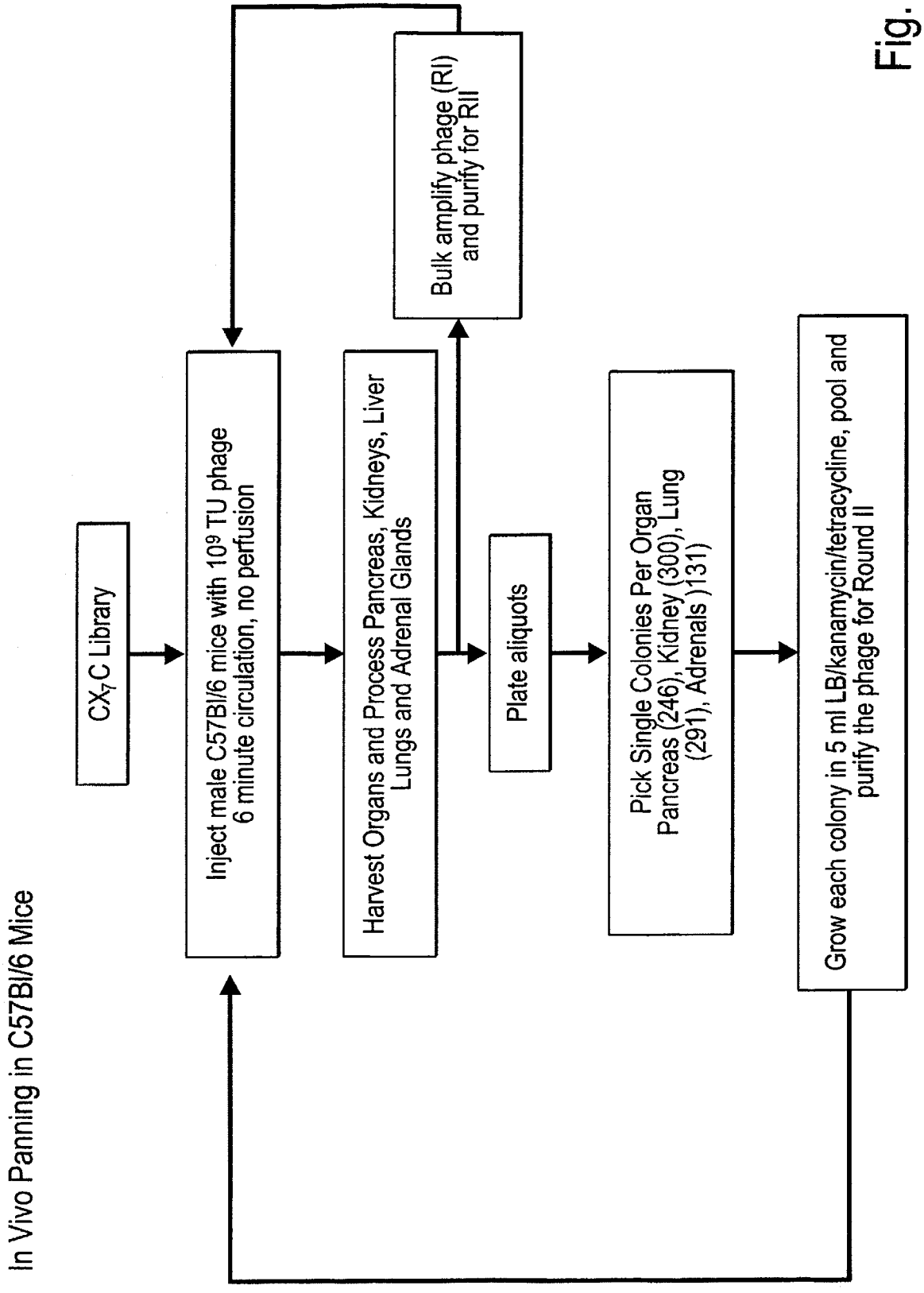
In Vivo Panning in C57Bl/6 Mice
CX7C Library
Inject male C57Bl/6 mice with 10^9 TU phage
6 minute circulation, no perfusion
Harvest Organs and Process Pancreas, Kidneys, Liver
Lungs and Adrenal Glands
Bulk amplify phage (RI)
and purify for RII
Plate aliquots
Pick Single Colonies Per Organ
Pancreas (246), Kidney (300), Lung
(291), Adrenals)131)
Grow each colony in 5 ml LB/kanamycin/tetracycline, pool and
purify the phage for Round II

Fig. 26

Phage and Phage DNA Recovery Schemes from PALM Catapulted Material

K91 Infection

- Catapult 90-120 islets and control sections into 30 µl protease cocktail in PBS within 48 hours. Protease cocktail: AEBSF, aprotinin, leupeptin, TPCK, elastase inhibitor, pepstatin A.
- Pool thawed samples and adjust final volume to 200 µl with PBS.
- Infect with 1 ml K91 for 2 hours at RT.
- Add LB/kanamycin/tetracycline 1:1 where the final [tetracycline] = 0.2 µg/ml. Let samples recover in the dark for 40 minutes to 1 hour.
- Increase [tetracycline] to 40 µg/ml and incubate overnight at 37 °C with agitation.
- Plate onto LB/kanamycin/tetracycline plates the following day.
- Pick single colonies to PCR amplify with fUSE5 primers for sequencing.

DNA Amplifications/Subcloning

- Catapult 90-120 islets into 30 µl 1 mM EDTA, pH 8.
- Pool thawed samples and concentrate.
- PCR1: PCR amplify peptide coding sequence with fUSE5 primers.
- PCR2; PCR amplify peptide coding sequence with nested primers.
- Sequence PCR2 products with M13 reverse primer.
- PCR3: PCR amplify peptide coding sequence with library primers containing SfiI sites.
- Digest gel-purified PCR products with SfiI. Also digest fUSE5 with SfiI/CIAP. Clean up products with Qiagen Qiaquick and Nucleotide Cleanup Kits.
- Ligate, electroporate into MC1061, and plate onto LB/streptomycin/tetracycline plates.
- Pick single colonies to PCR amplify with fUSE5 primers for sequencing.

Fig. 27

Islet Homing Peptide Sequence Homology

Peptide Sequence	Homologous Protein	Sequence	Amino Acid Residue	Sequence Identity	Expected Value
CVSNPRWKC	putative mouse protein (cloned from full length mouse gene encyclopedia project)	VSNPRW	123-128	100% (6/6)	6.7
	PI3-kinase p110 subunit	SNPRW	379-383	100% (5/5)	53
	rat endothelin-converting protein	PRWK	422-425	100% (4/4)	90
	TNF Receptor p60 homologue 1	VSNPRW	130-136	85% (6/7)	127
	121 kDa protein isolated from rat adipocytes containing insulin-regulated glucose transporter GLUT4	NPRW	293-296	100% (4/4)	308
	Reg2 (present in regenerating pancreatic islets and normal exocrine pancreas)	SNRRW	114-118	80% (4/5)	391
	ephrin-related receptor tyrosine kinase ligand 4 (LERK 4)	SNPR	35-38	100 (4/4)	524
CVPRRWDVC	laminin β-2 chain	PRRWD	197-201	100 (5/5)	6.4
CQHTSGRGC	dihydropyridine sensing L-type Ca2+ channel, β3-subunit laminin β-2 chain	QHTSG	442-446	100 (5/5)	90
		TSGRG	1088-1092	100 (5/5)	218
CRARGWLLC	α3 integrin	RAPGWLL	10-16	85 (6/7)	12

Fig. 28

Islet Homing Peptide Sequence Homology

Peptide Sequence	Homologous Protein	Sequence	Amino Acid Residues	Sequence Idenity	Expected Value
CGGVHALRC	Ret receptor	VHALR	53-57	100 (5/5)	309
	putative mouse protein	GGVHSL GVDALR	432-437 248-253	99 (6/6) 83 (5/6)	556 2416
	RIKEN cDNA	GVHAL	58-62	100 (5/5)	556
CFNRTWIGC	chloride channel protein	NRTWV	411-415	100 (5/5)	50
	tyrosine protein kinase receptor FLK-2	FHRTW	711-715	100 (5/5)	67
CSRGPAWGC	Bone morphogenic protein 3B, growth differentiation factor 10 (TGF-β family member)	RGPSW	32-36	100 (5/5)	121
	5-HT 6 receptor	GPAW	13-16	100 (4/4)	218
	Reticulon 1, neuroendocrine specific protein	PAWG	45-48	100 (4/4)	218
CWSRGQGGC (25% I vs. 2.2%C)	SOX1 SOX2 SOX3 SOX14	WSRGQ	61-65 53-57 79-83 3-7	100 (5/5)	21 21 21 21
	endothelin-1 receptor	WSRVQG	92-97	83 (5/6)	90
	DAP 12, tyrosine kinase binding protein	SRGQG	71-75	100 (5/5)	163
	excitatory AA symporter (L-E, L, D-D/Na^+)	SRGRGG	551-556	99 (6/6)	527

Fig. 29

Islet Homing Peptide Sequence Homology

Peptide Sequence	Homologous Protein	Sequence	Amino Acid Residues	Sequence Identity	Expected Value
CLASGMDAC (9.5%)	TNF-α	LANGMD	116-121	99 (6/6)	50
CHDERTGRC (8%)	SOX6	HDQRT	274-278	99 (6/6)	218
	PI3 kinase p85 subunit	HEERT	611-615	100 (5/5)	163
CAHHALMEC (6%)	APC Protein	ALMEC	569-573	100 (5/5)	15
CMQGARTSC (6%)	cathespsin W (thiol protease)	ARTSC	365-369	100 (5/5)	67
	α2 adrenergic receptor	QGART	326-330	100 (5/5)	121
	Pancreatitis-associated protein Reg 3α	RTSC	37-40	100 (4/4)	393

Fig. 30

Islet Homing Peptide Sequence Homology

Peptide Sequence	Homologous Protein	Sequence	Amino Acid Residues	Sequence Idenity	Expected Value
CHVLWSTRC (13% I vs. 2.2%c)	integrin linked protein kinase	VLKVRDWSTR	220-230	60 (6/10)	122
	Ephrin-A2 receptor tyrosine kinase ligand 6 (LERK 6)	VLWS	202-205	100 (4/4)	220
	α3a integrin	VLWS	147-150	100 (4/4)	220
CMSSPGVAC (10.7% I vs 3.2%C)	insulin receptor substrate 1	MSPGVA MASP	611-616 1-4	6/7 4/4	164 2308
	laminin α5 chain	SSPGV	467-471	100 (5/5)	220
	angiopoietin-2 receptor	MSSP	262-265	100 (4/4)	265
	SOX17	MSSP	1-4	100 (4/4)	396
	citron protein (rho/rac binding protein-GTP form)	MNSPG	998-1002	100 (5/5)	396
	glucocorticoid receptor	SSPSVA SSPG	45-50 402-405	83 (5/6) 100 (4/4)	396 1720
CLGLLMAGC (13% I vs. 4.3%C)	chloride channel protein 2	LGLLMA	105-110	100 (6/6)	8.7
	tumor necrosis factor receptor 2	LGLLM	272-276	100 (5/5)	51
	histidine-rich membrane protein Ke4	LGLLVAG	21-27	99 (7/7)	51
	vascular endothelial-cadherin receptor	LGLLAVAAMAG	15-25	63 (7/11)	68
	endothelial protein C receptor	LGILM_GC LLLPGC	217-223 12-16	81 (7/8) 82 (5/6)	91 82
	Wnt-3 proto-oncogene	LGLLLSG	6-10	99 (7/7)	164

Fig. 31